

FIGURE 1

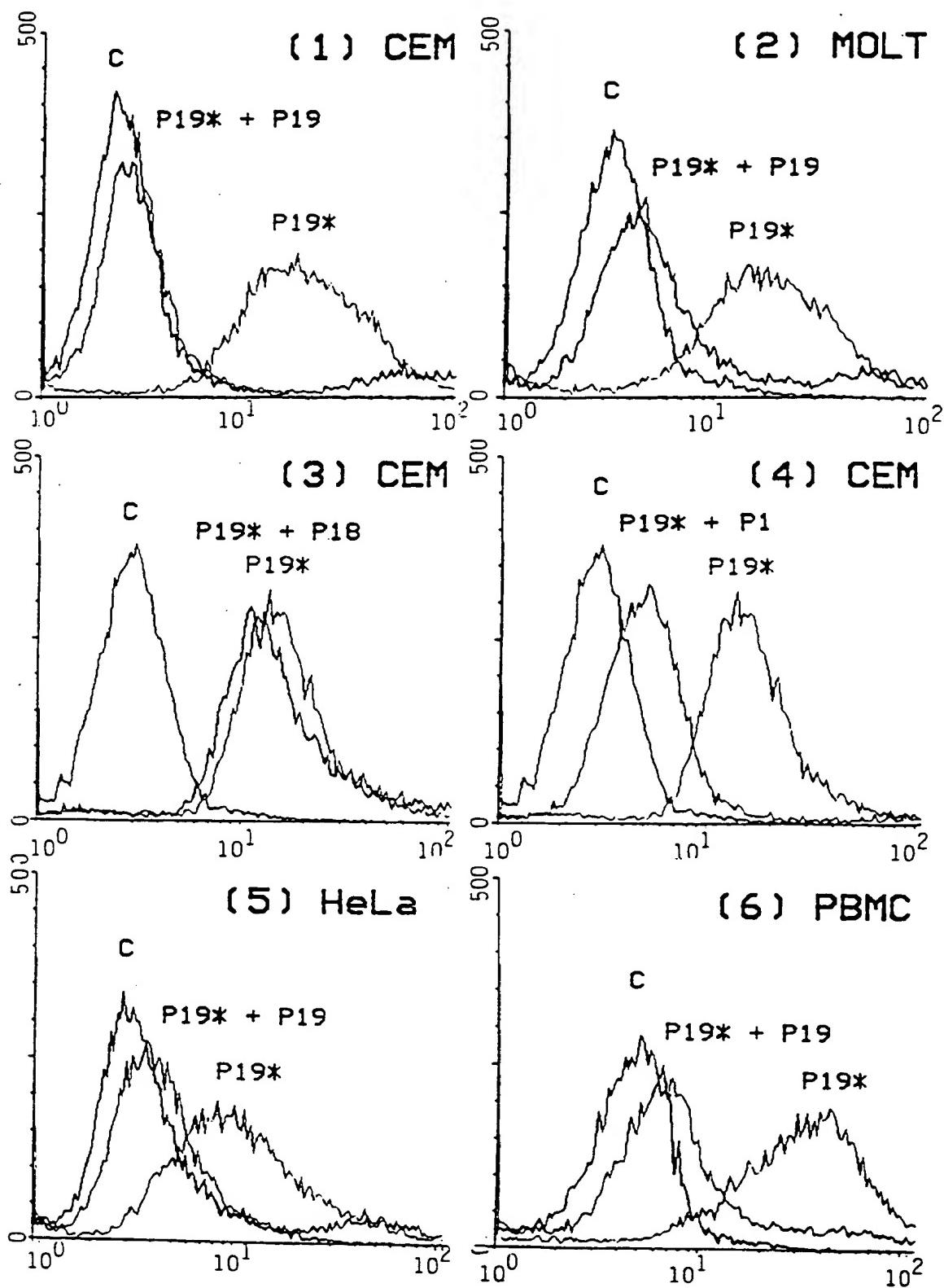


FIGURE 2

SELECTED PREFERENCES:

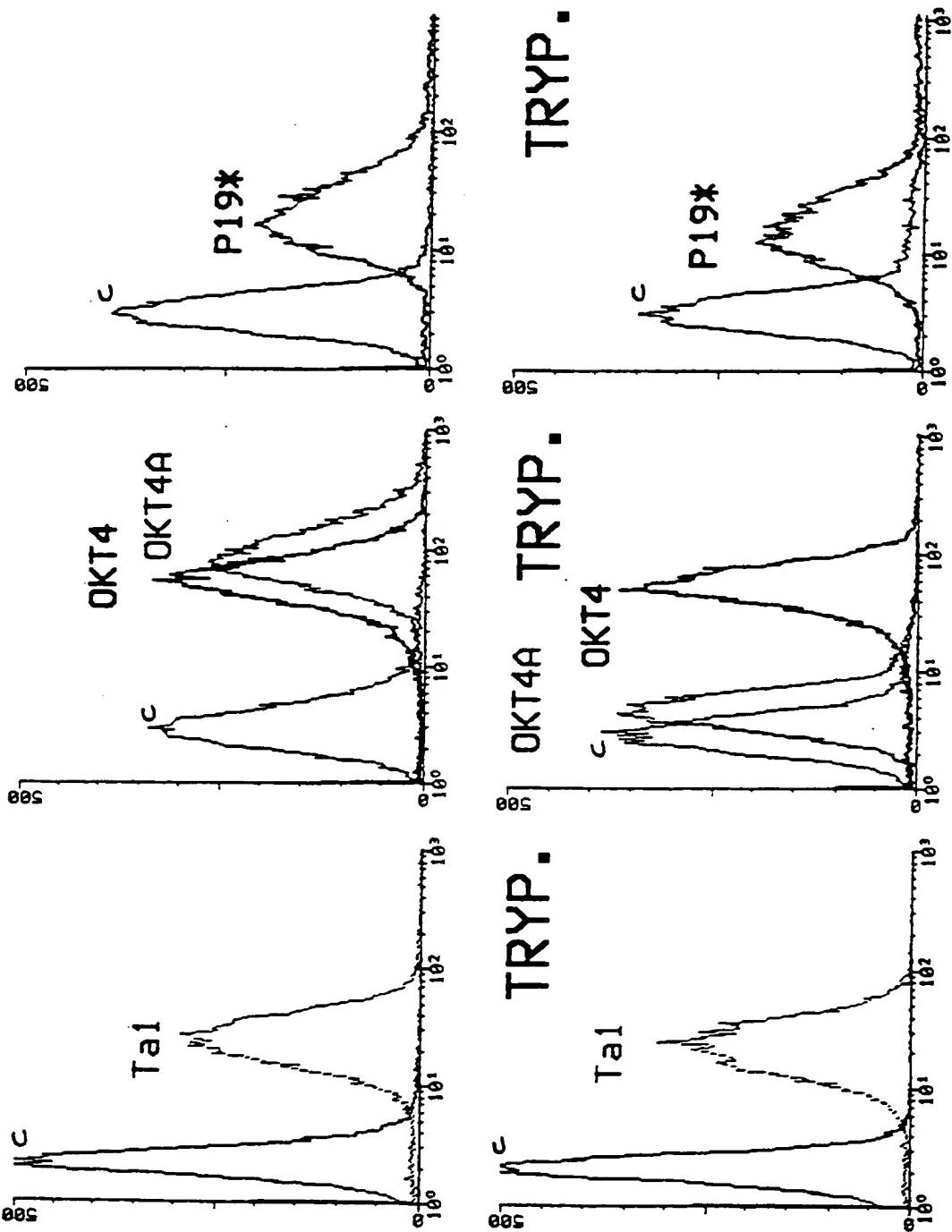


FIGURE 3A

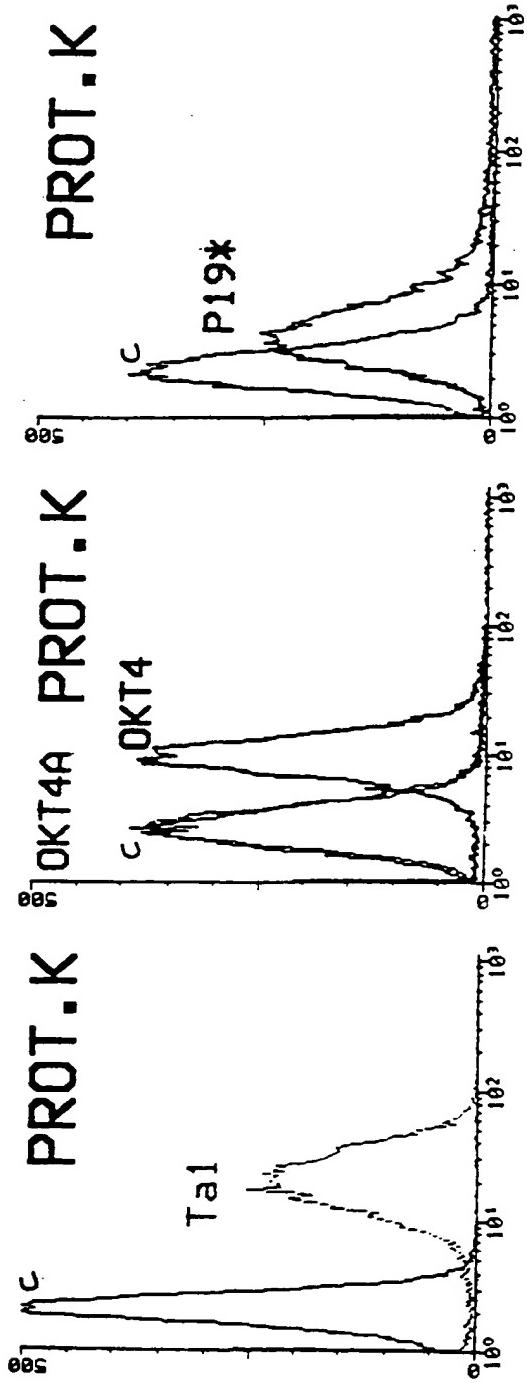


FIGURE 3B

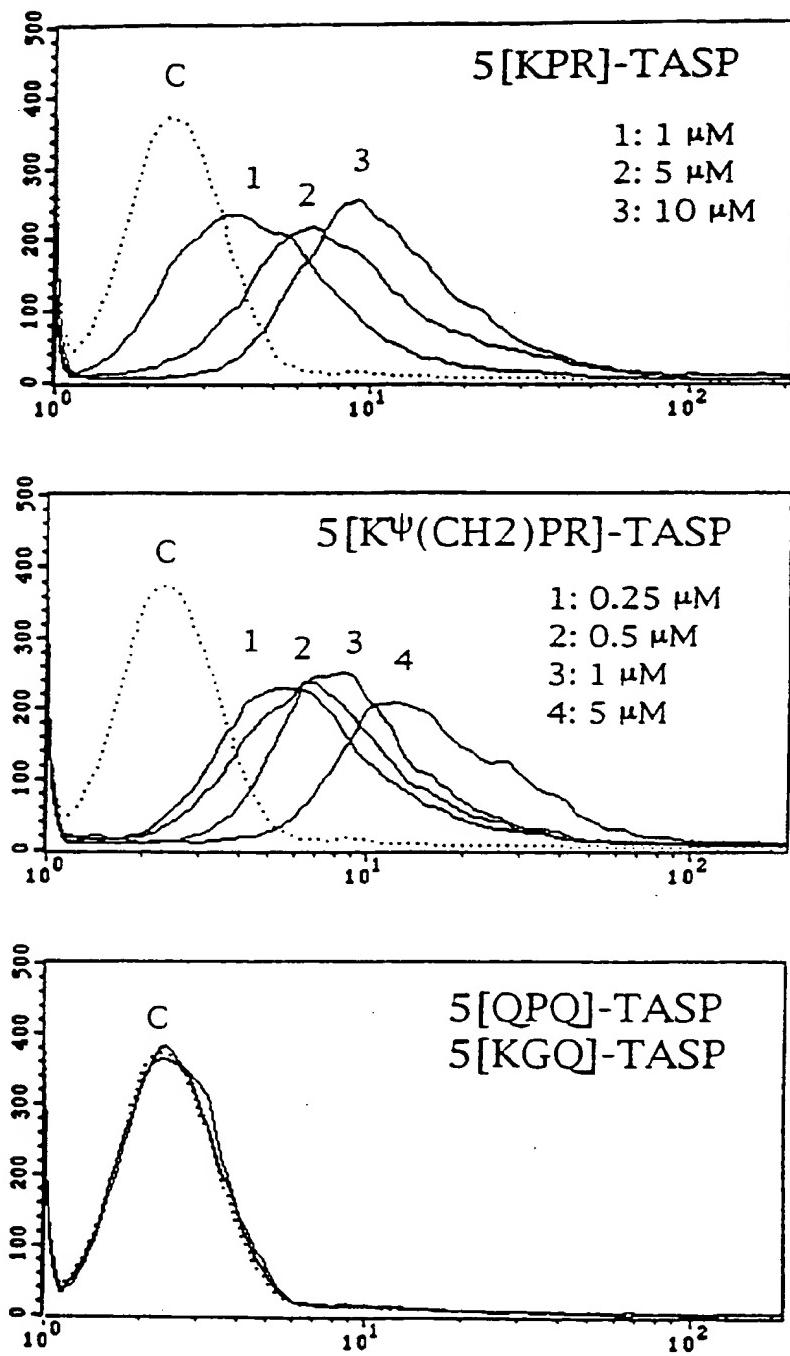


FIGURE 4

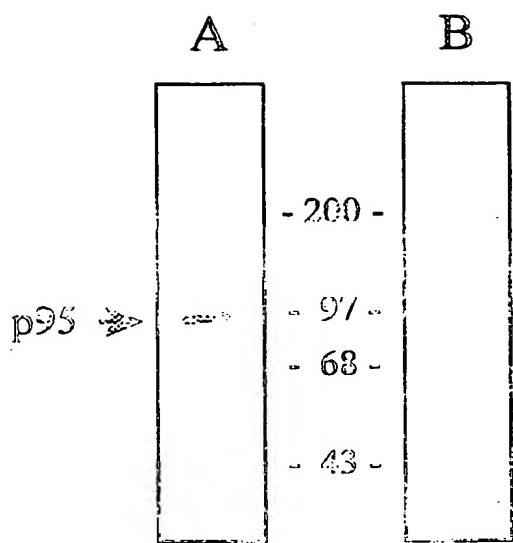


FIGURE 5

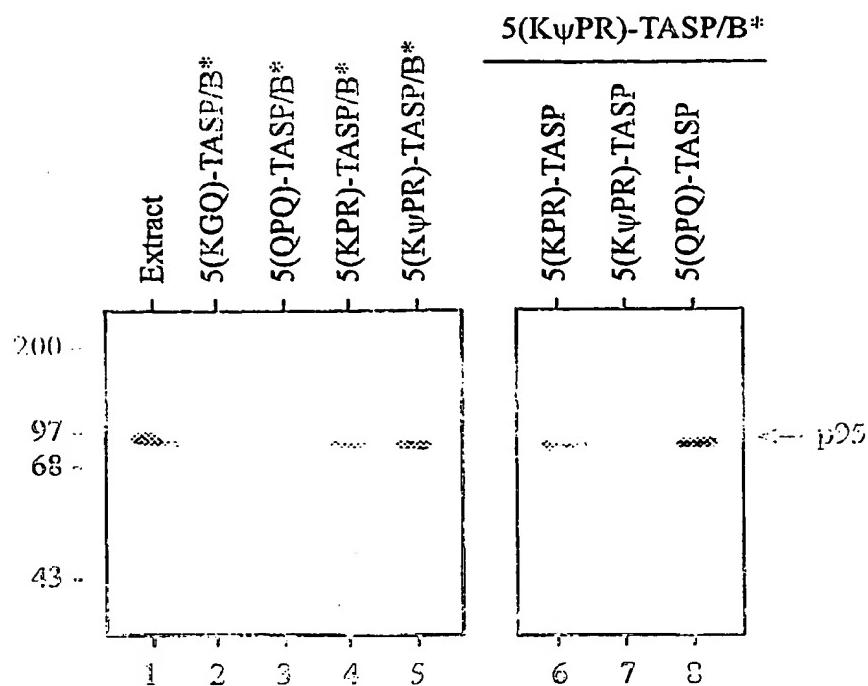


FIGURE 6

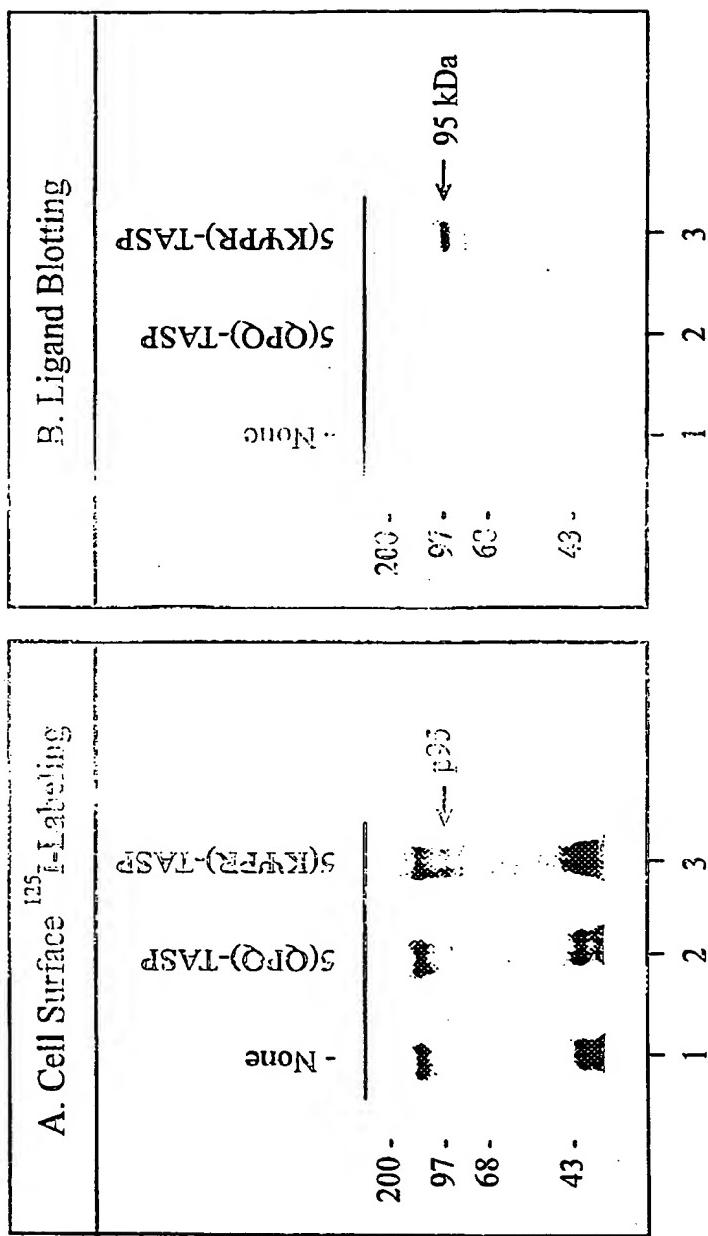


FIGURE 7

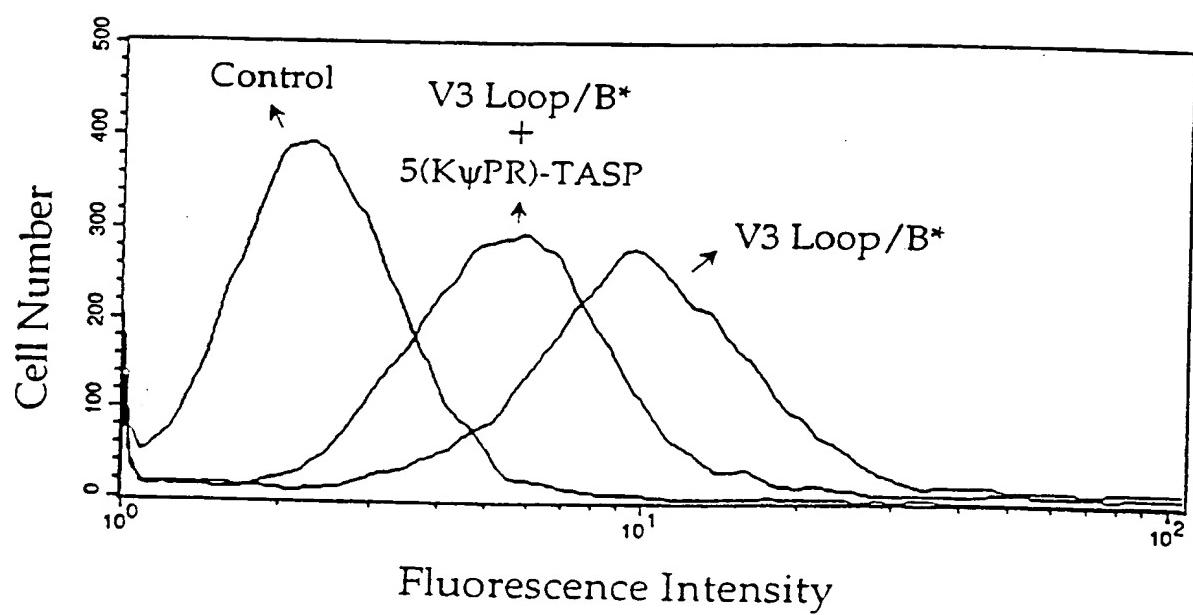


FIGURE 8A

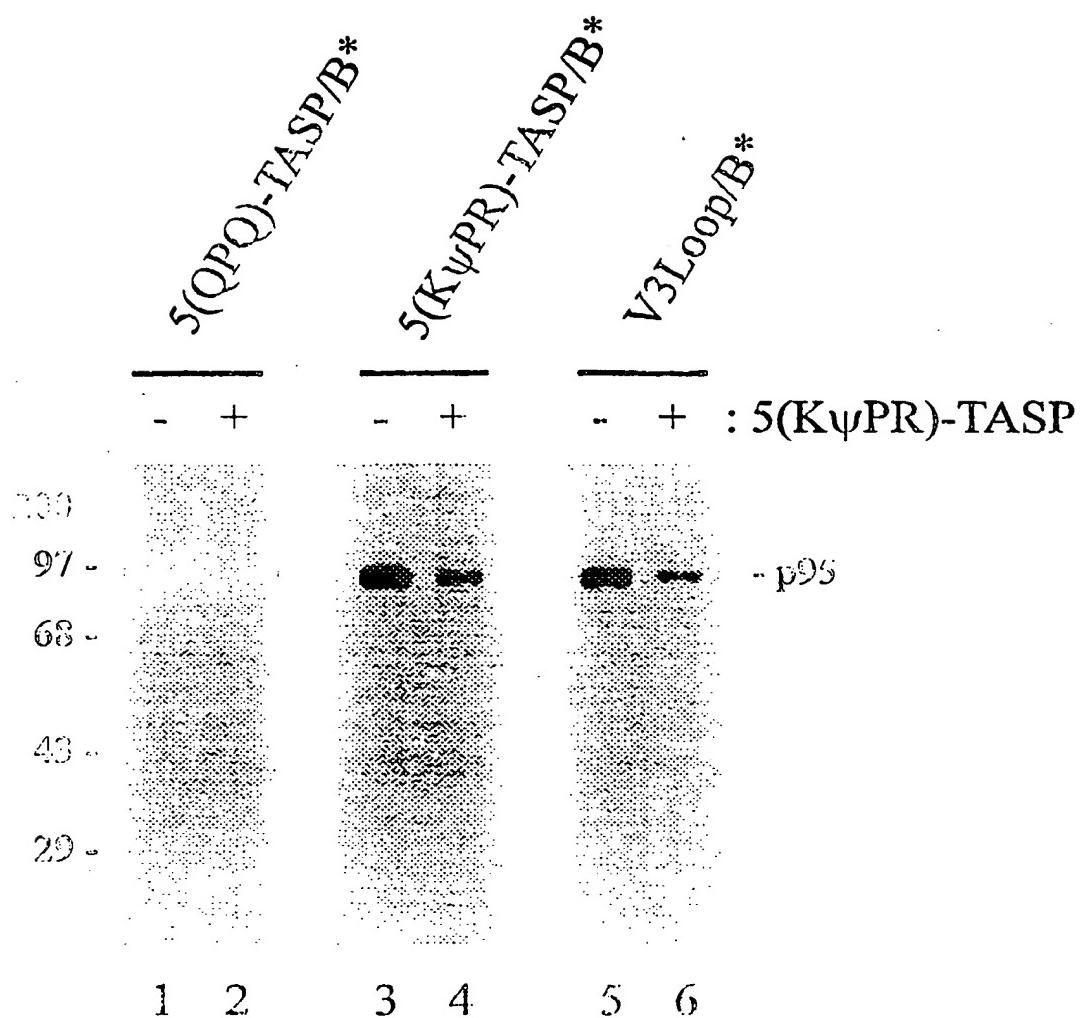


FIGURE 8B

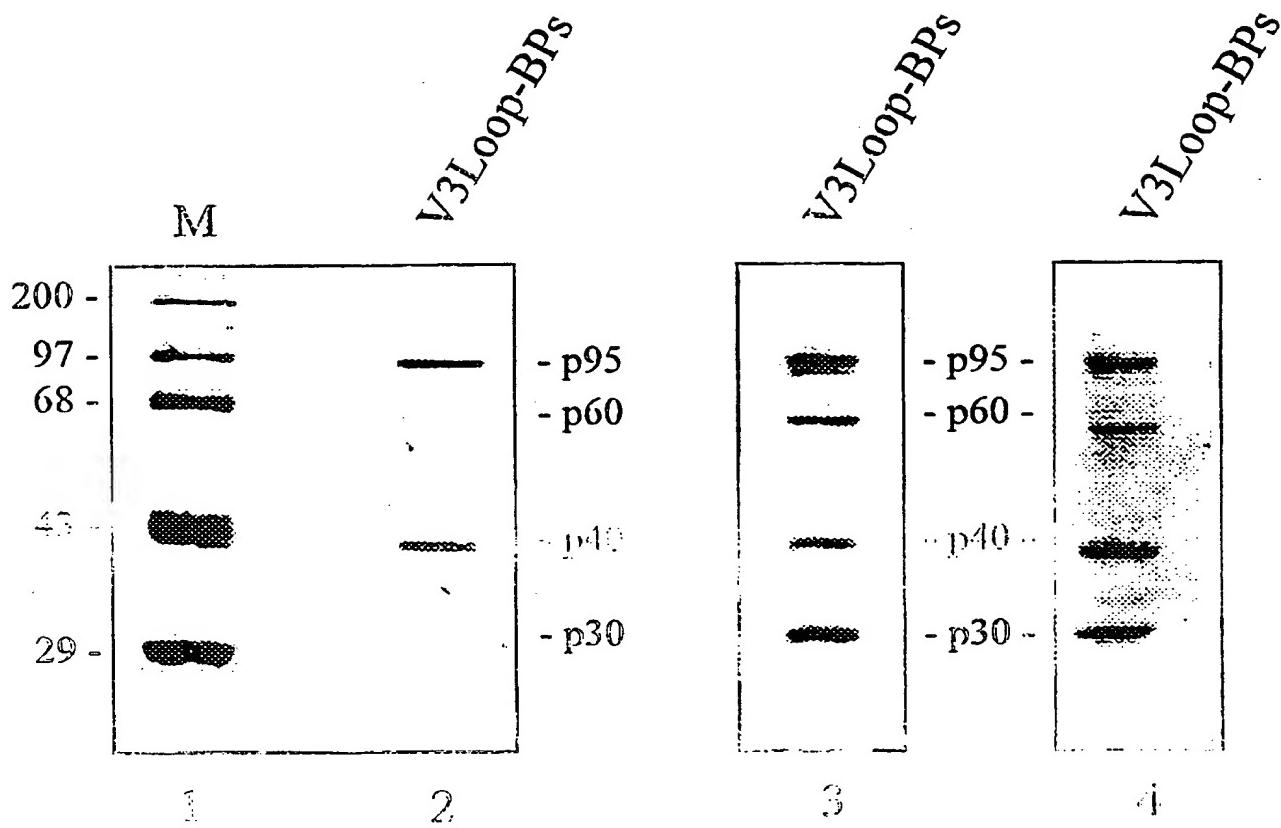
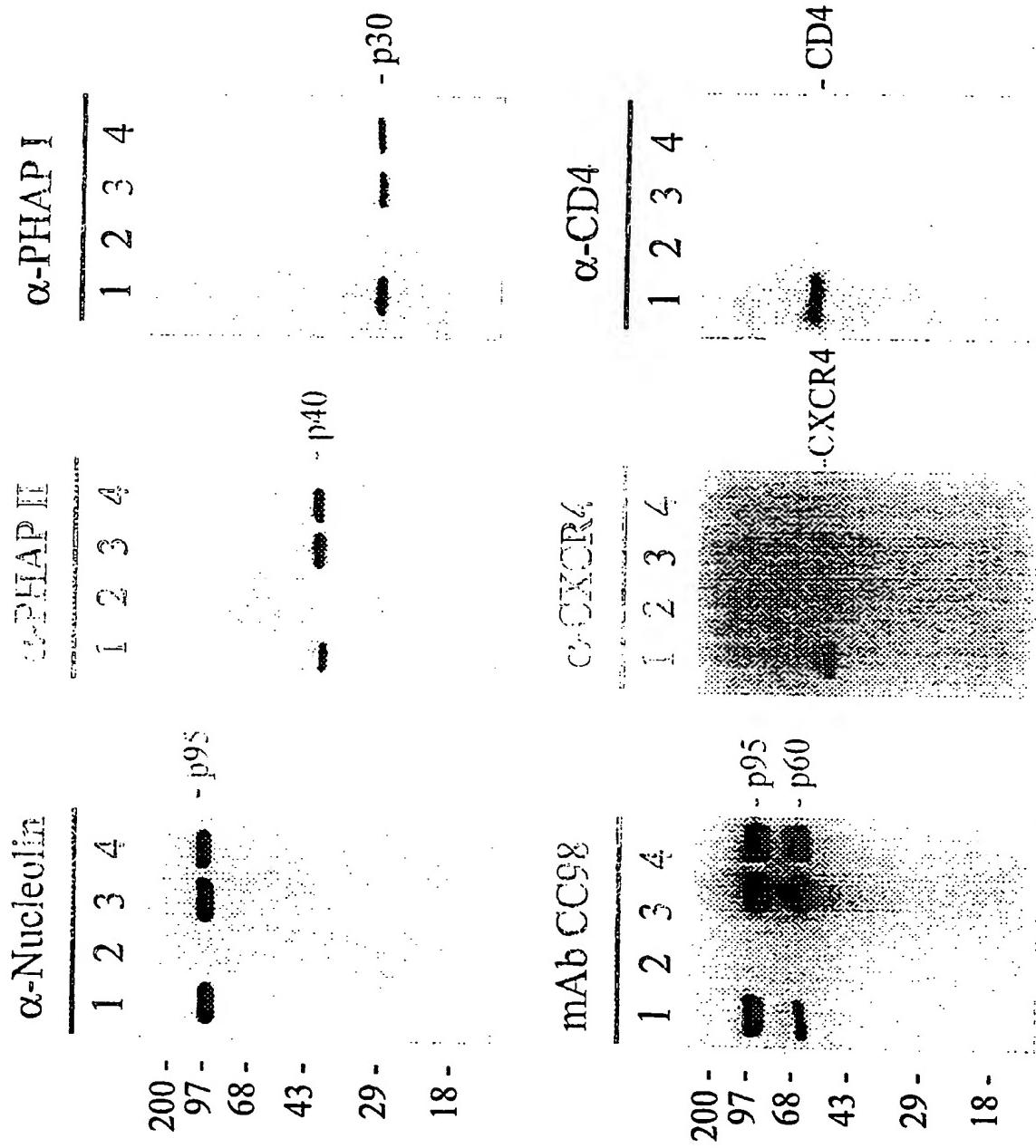


FIGURE 9



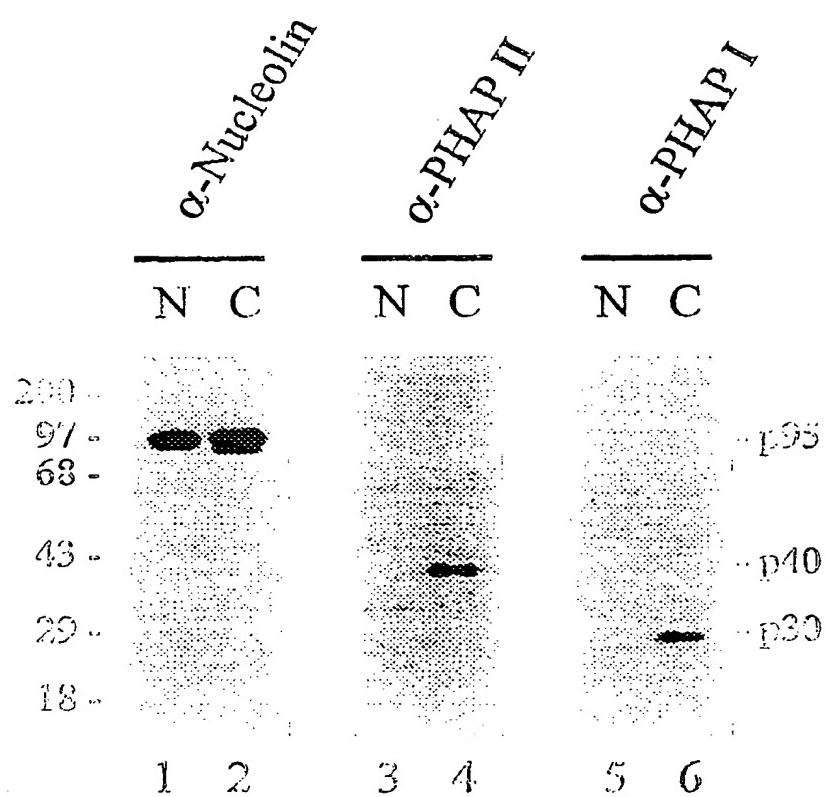


FIGURE 11

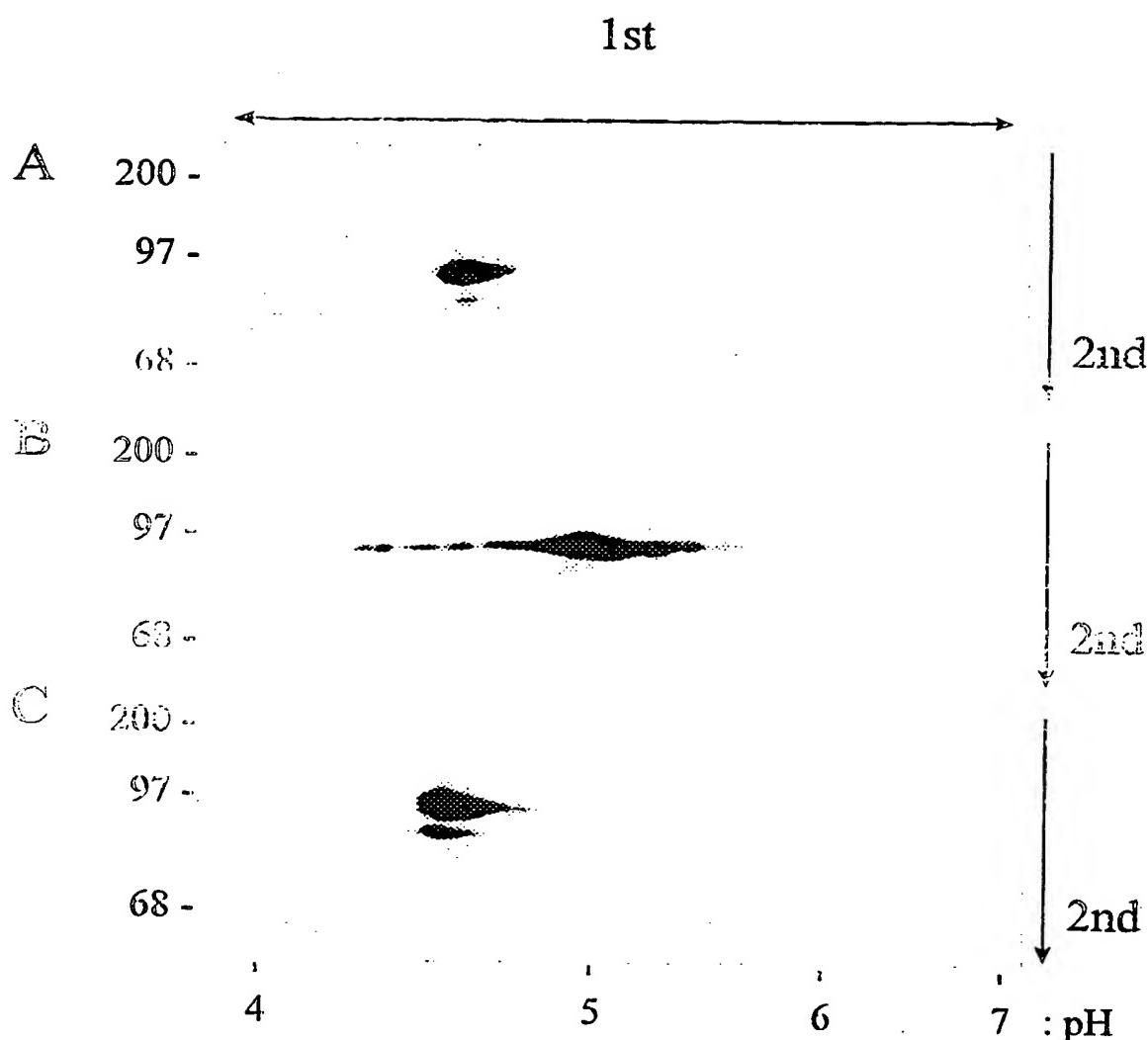


FIGURE 12

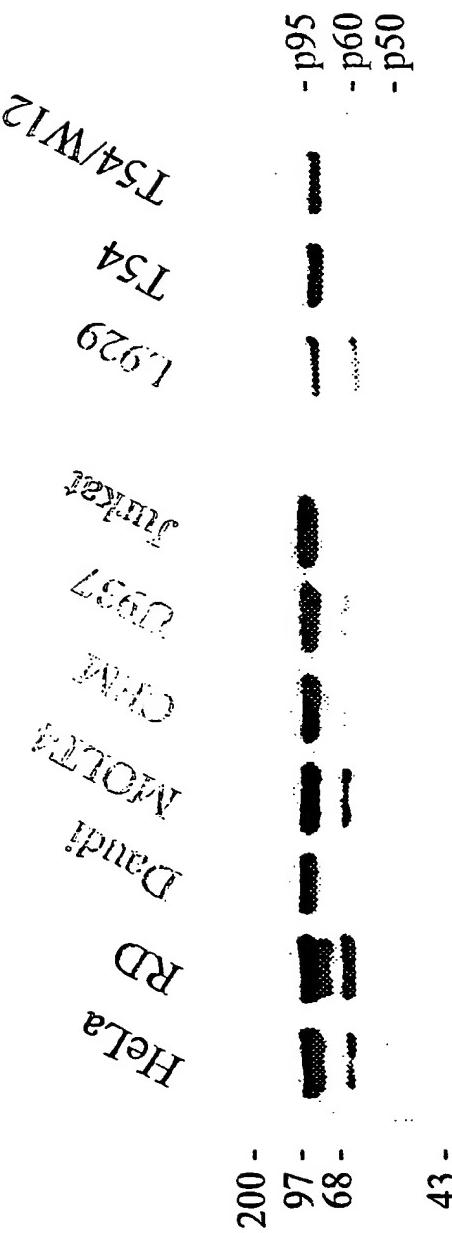


FIGURE 13A

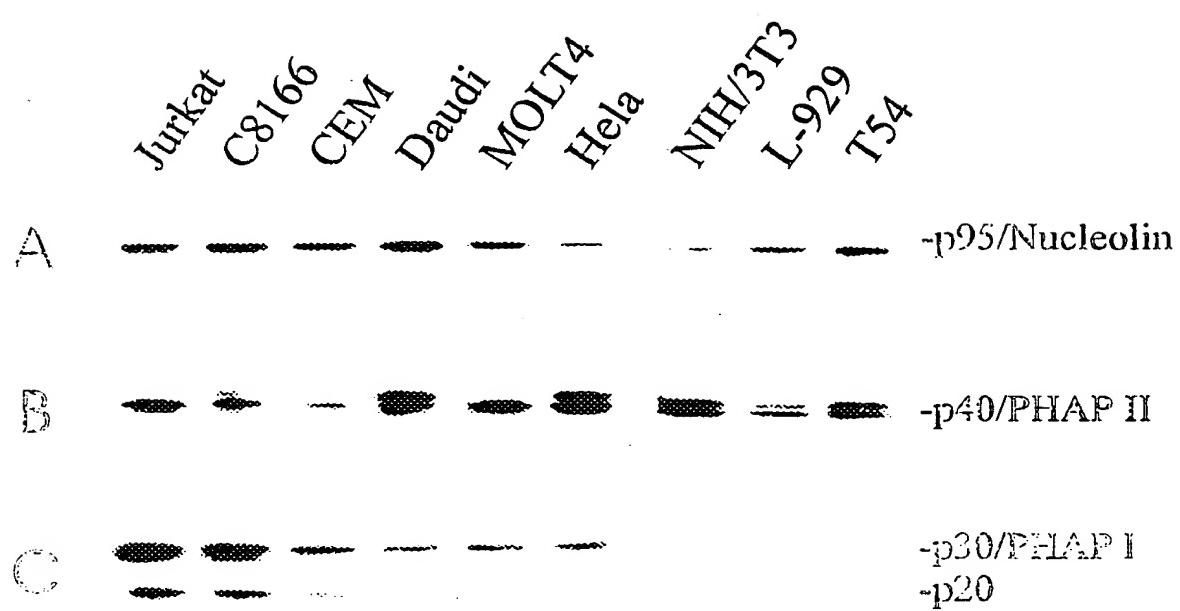
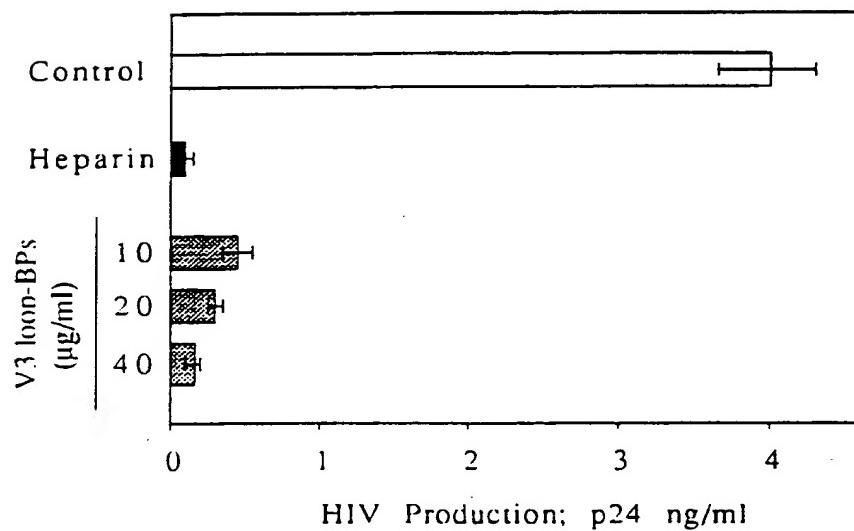


FIGURE 13B

A.



B.

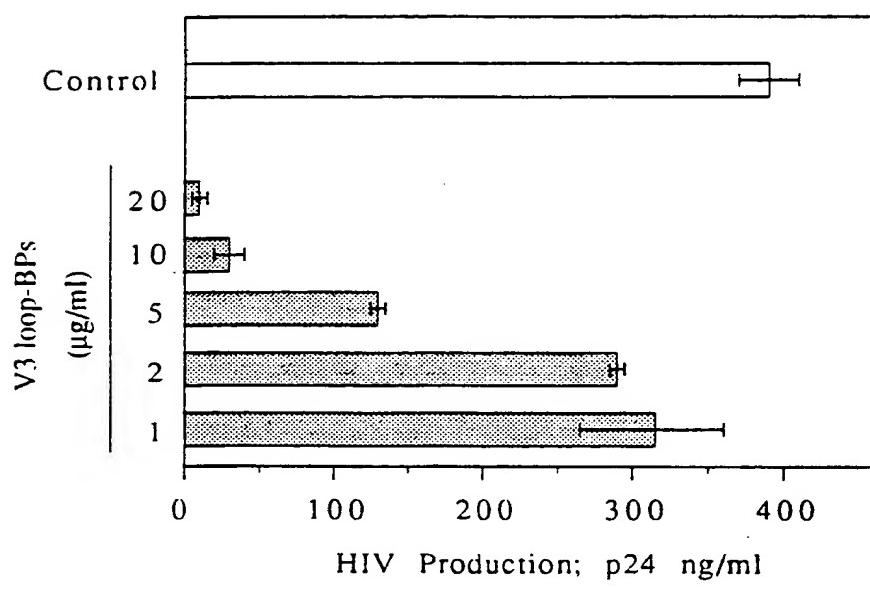


FIGURE 14

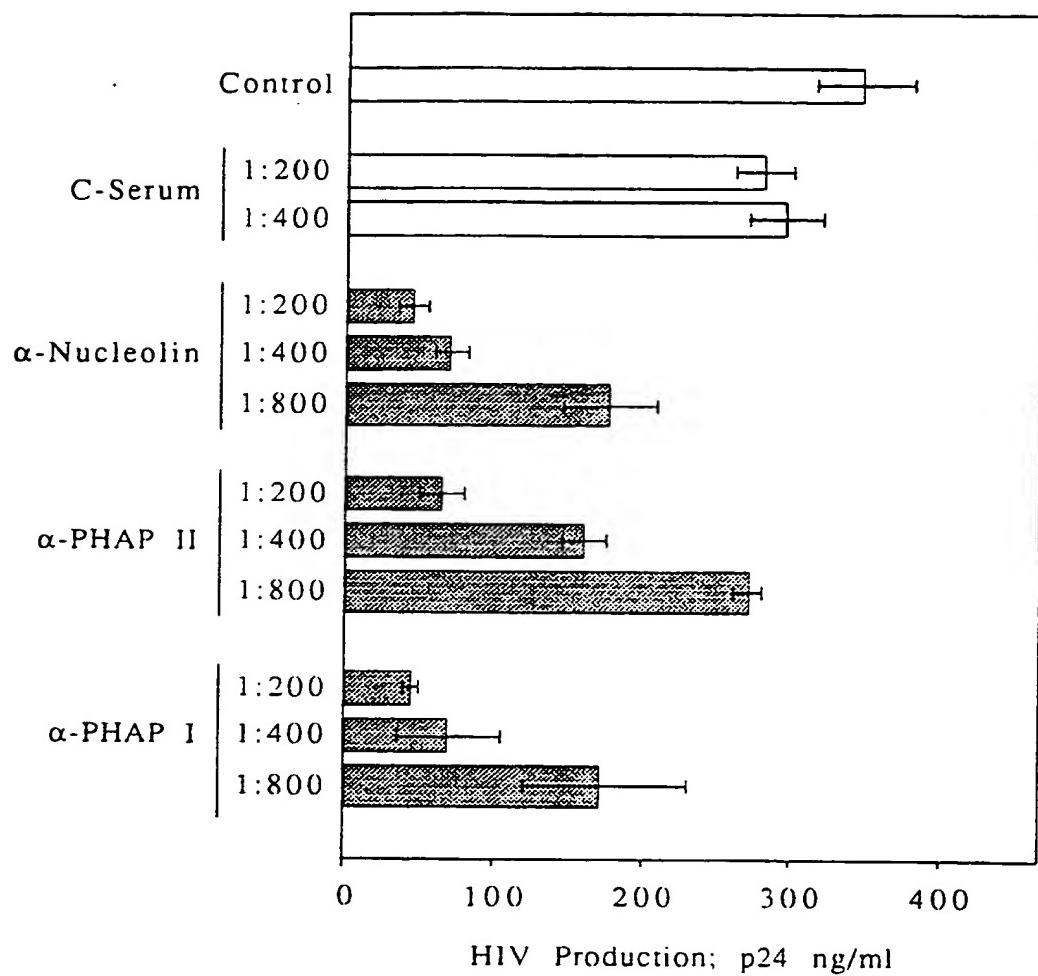
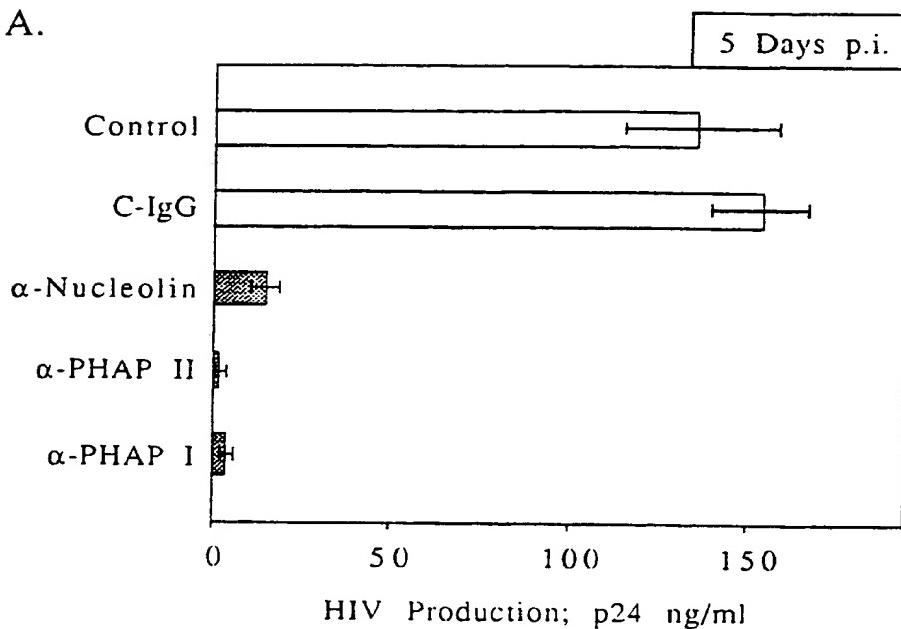


FIGURE 15

A.



B.

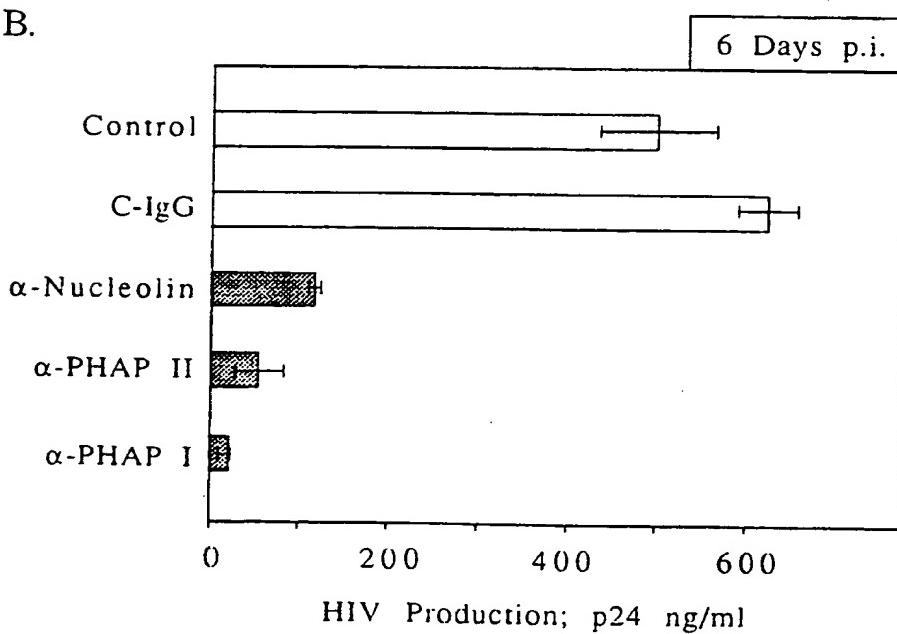


FIGURE 16

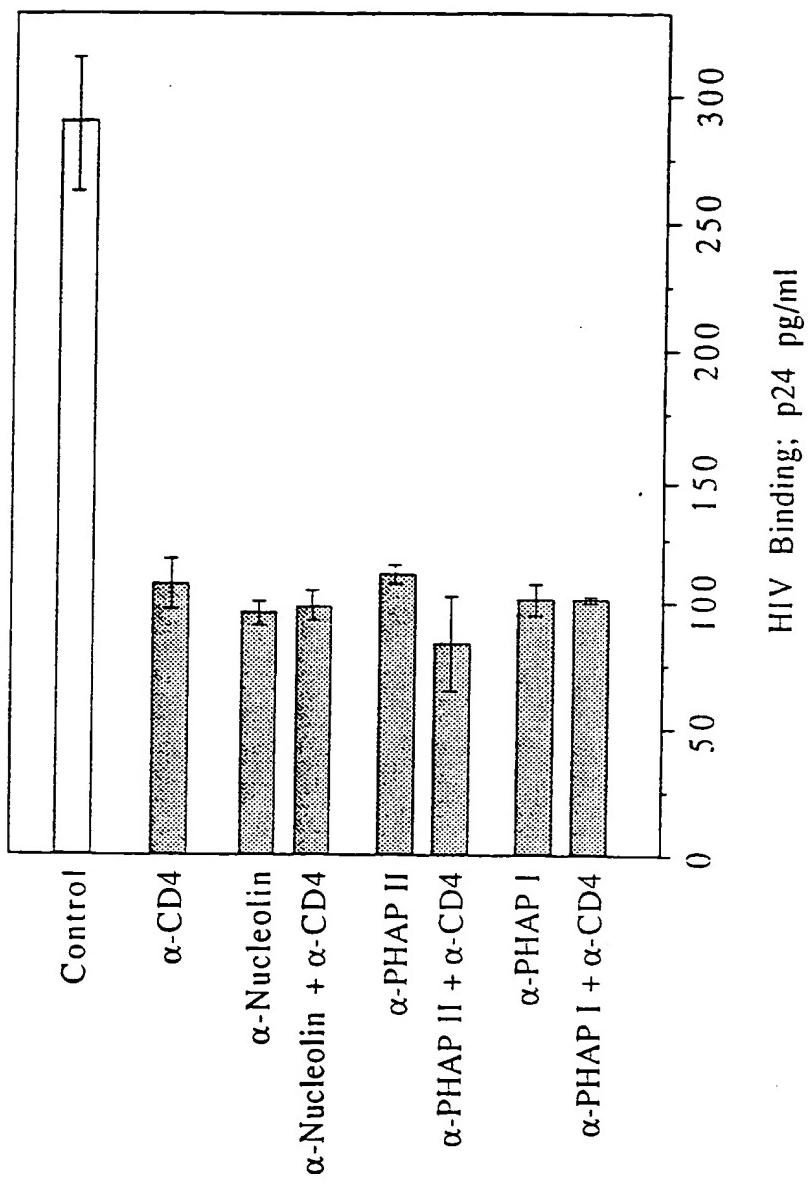


FIGURE 17

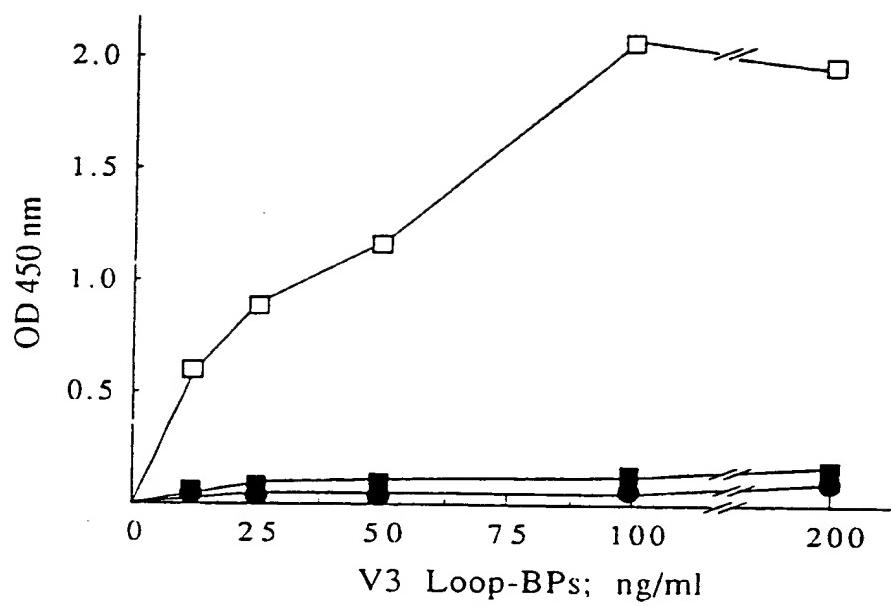
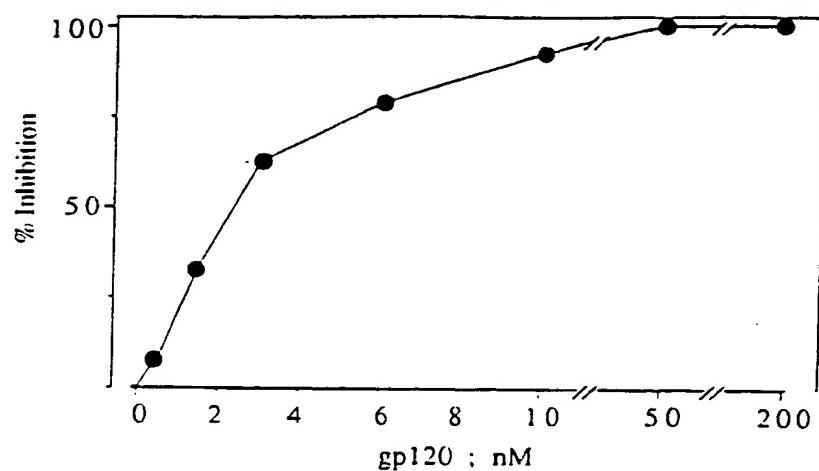
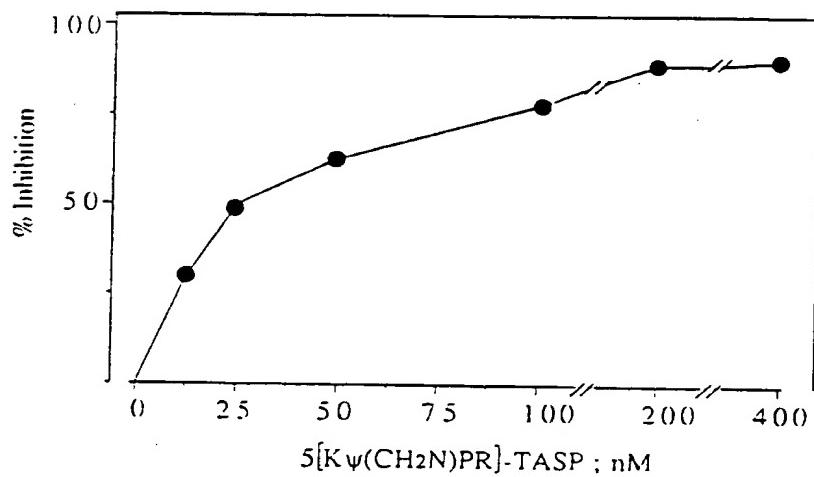


FIGURE 18

A. $5[\text{K}\psi(\text{CH}_2\text{N})\text{PR}]\text{-TASP}$ Binding to the V3 loop-BPs

B. gp120 Binding to the V3 loop-BPs



C. gp120 Binding to the V3 loop-BPs

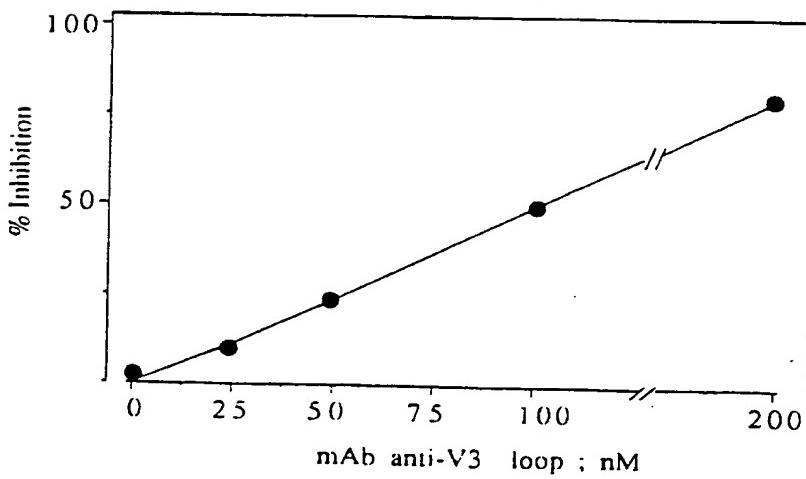


FIGURE 19

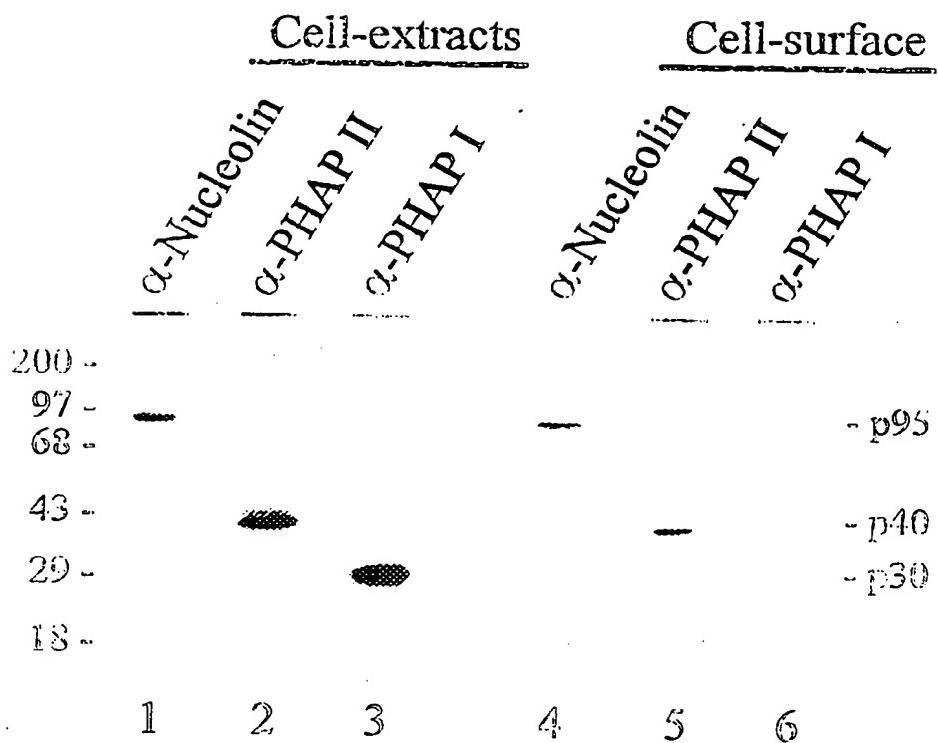


FIGURE 20

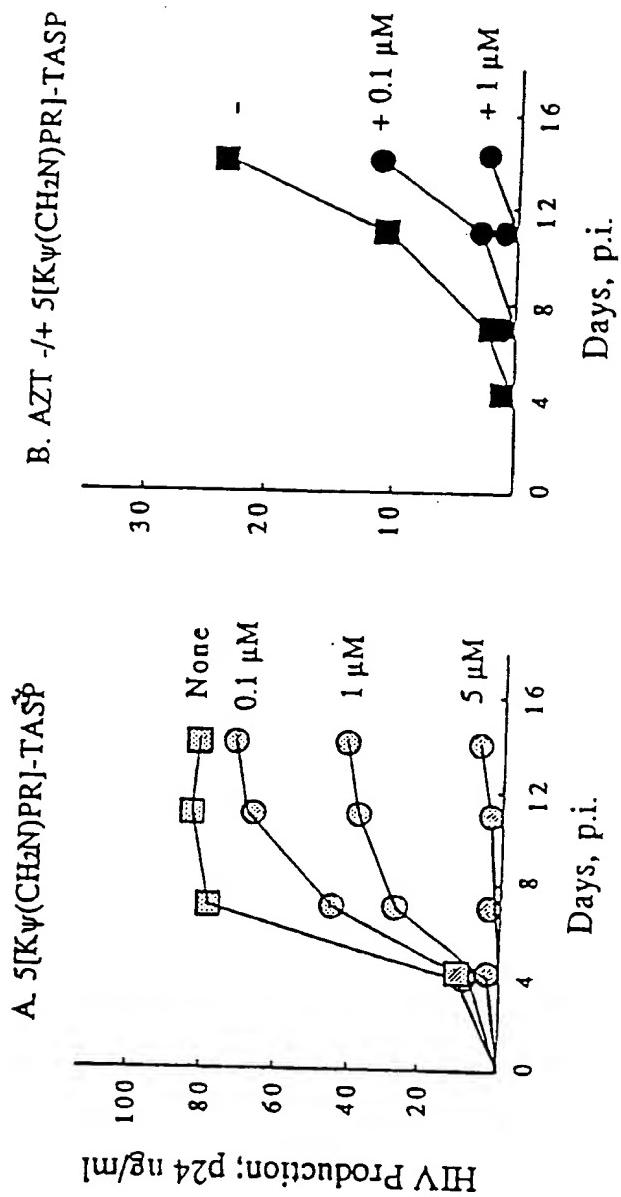


FIGURE 21

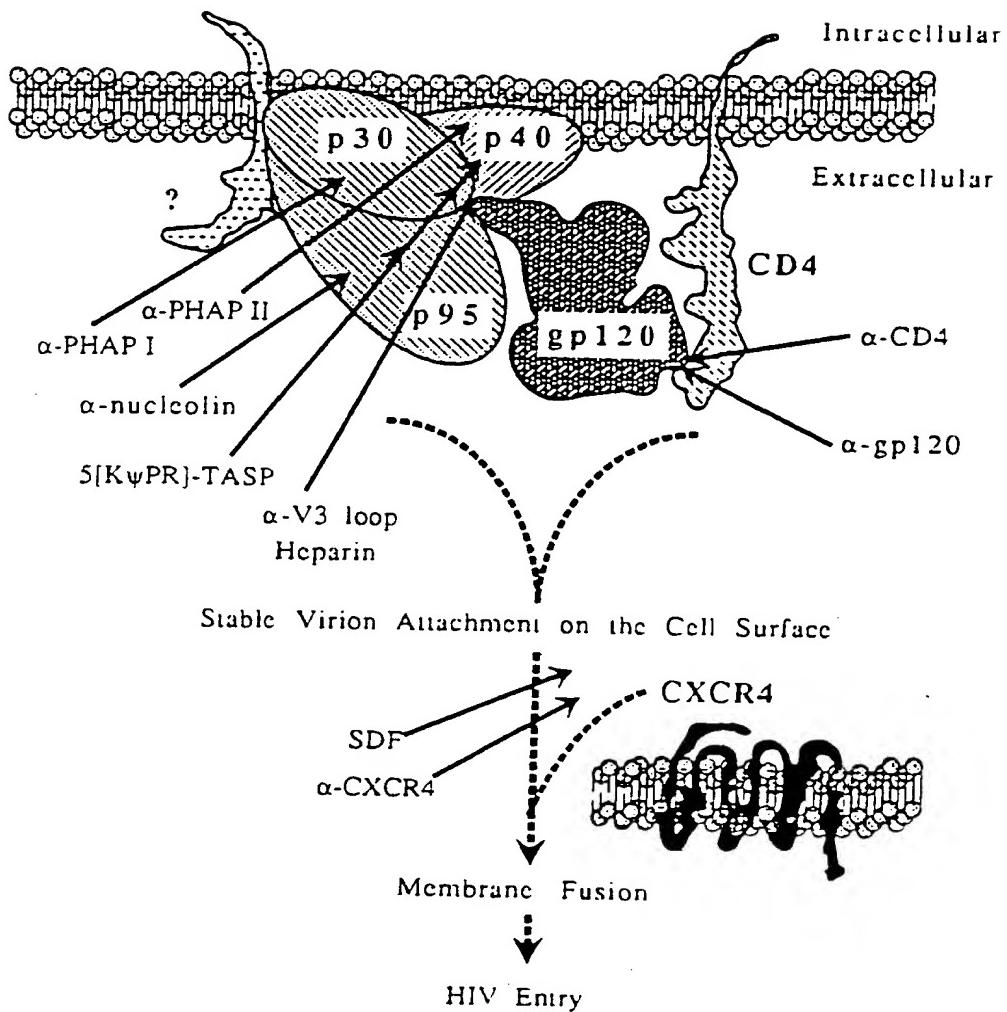


FIGURE 22

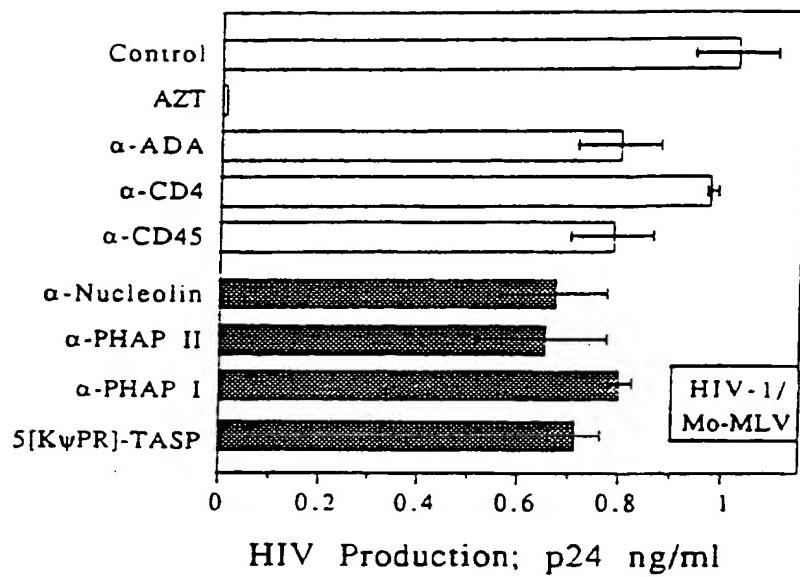


Figure 23

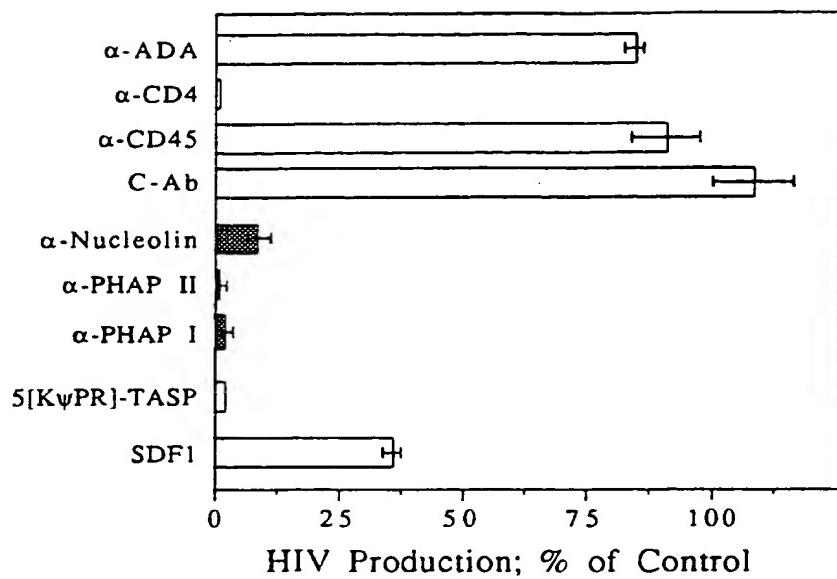


Figure 24

28 / 67

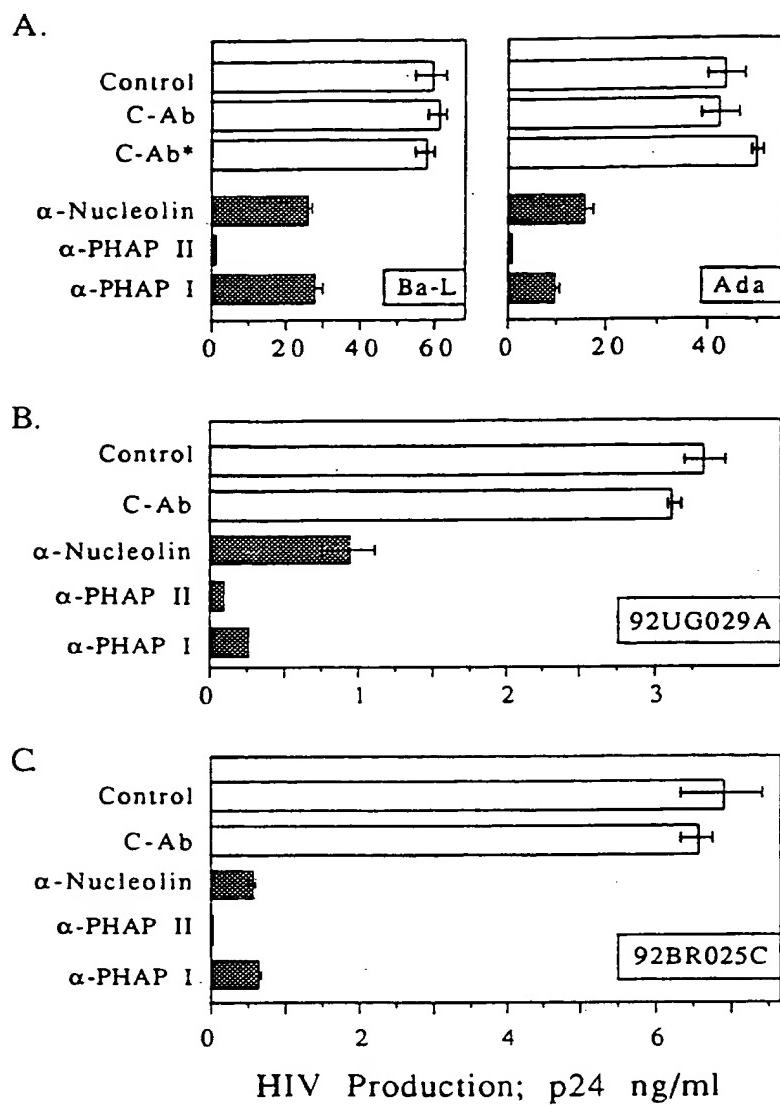


Figure 25

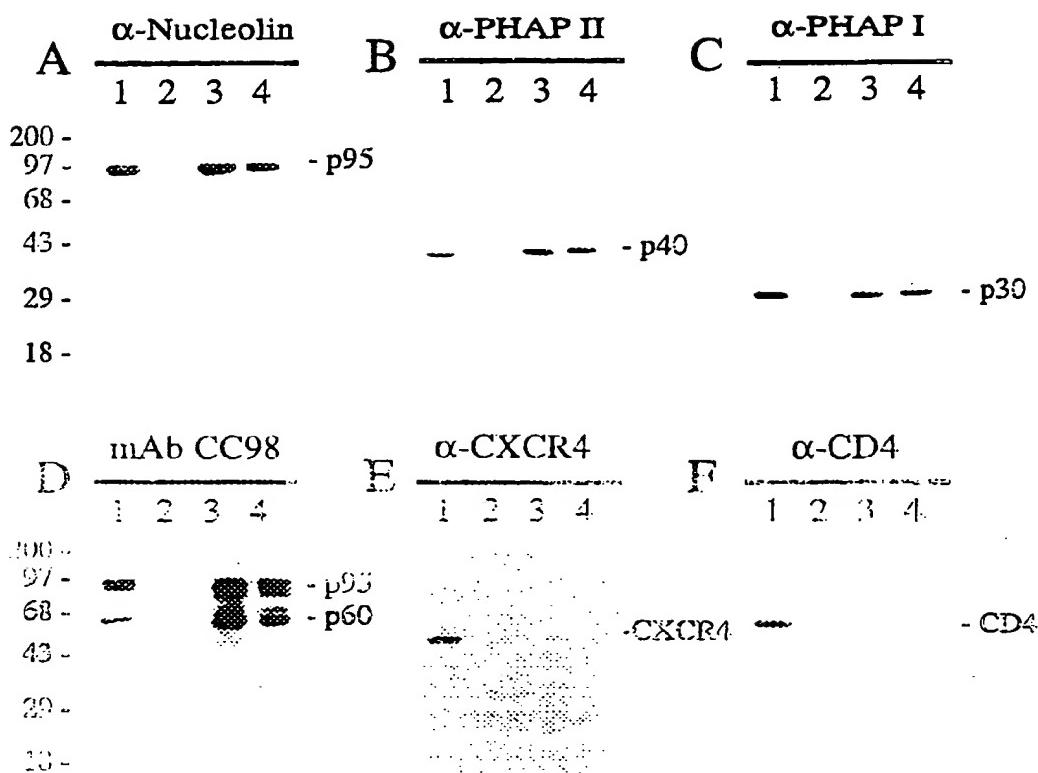


Figure 26

30 / 67

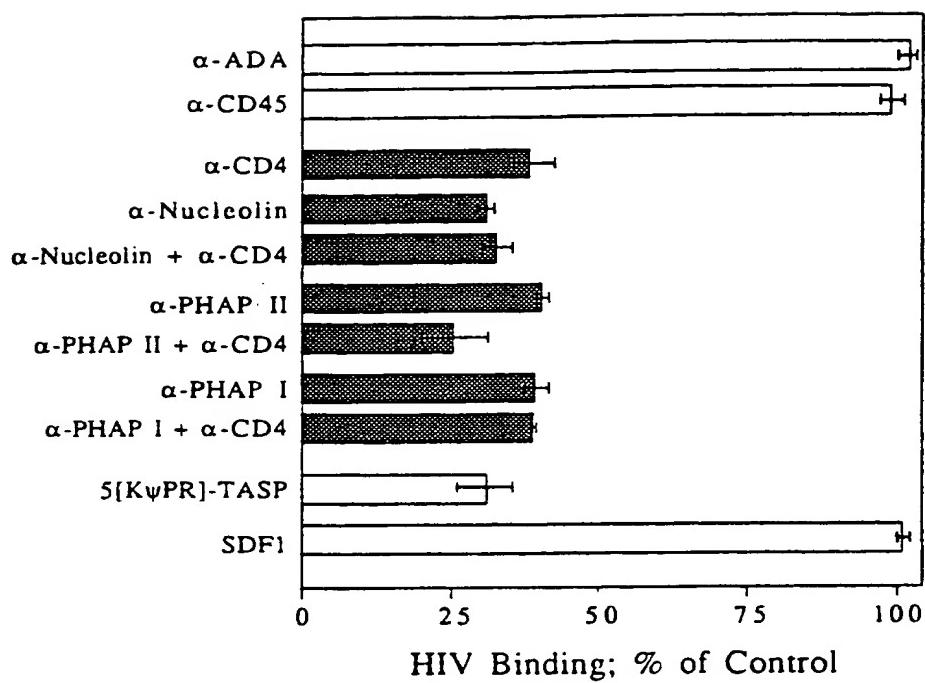


Figure 27

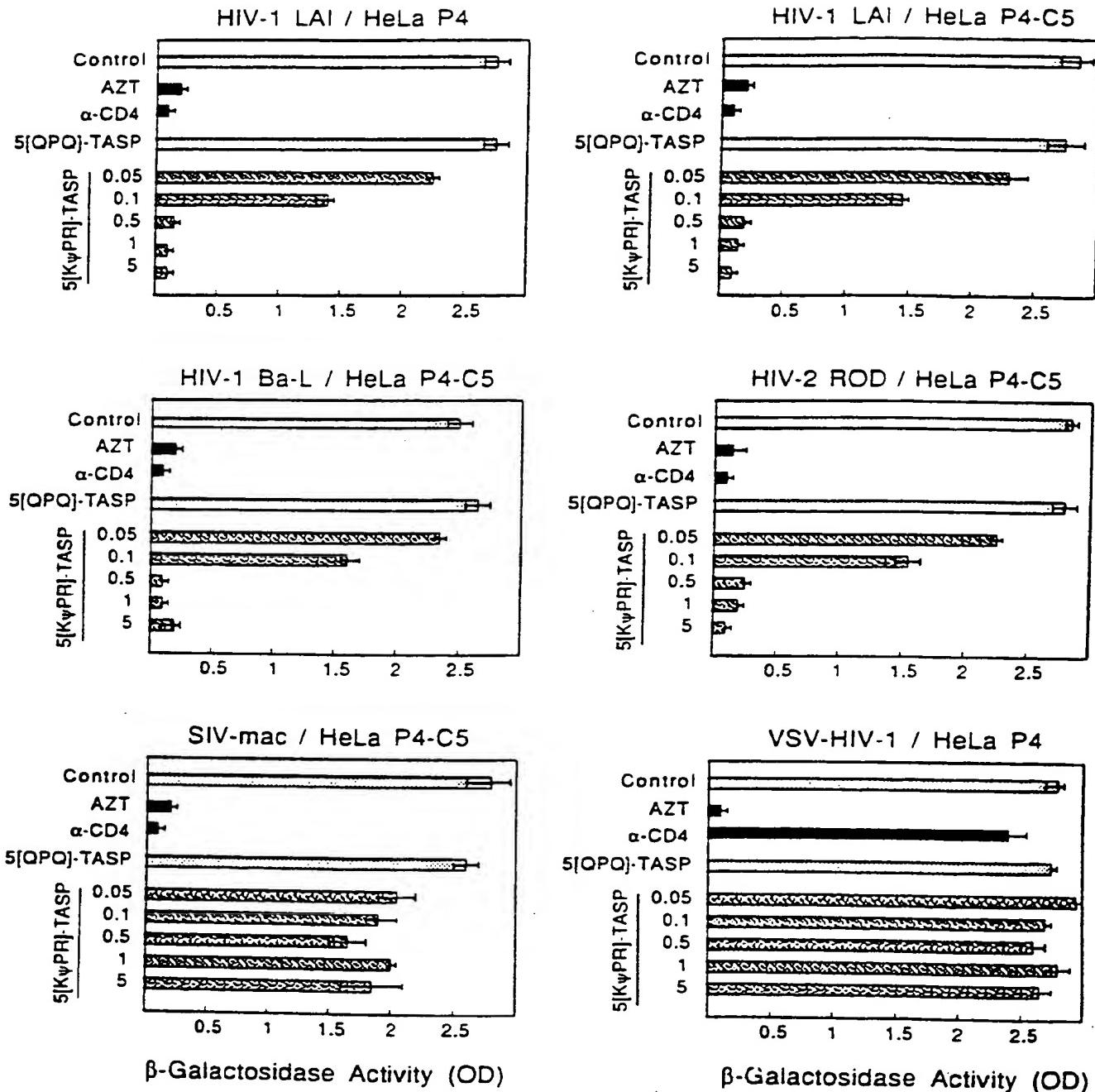


FIGURE 28

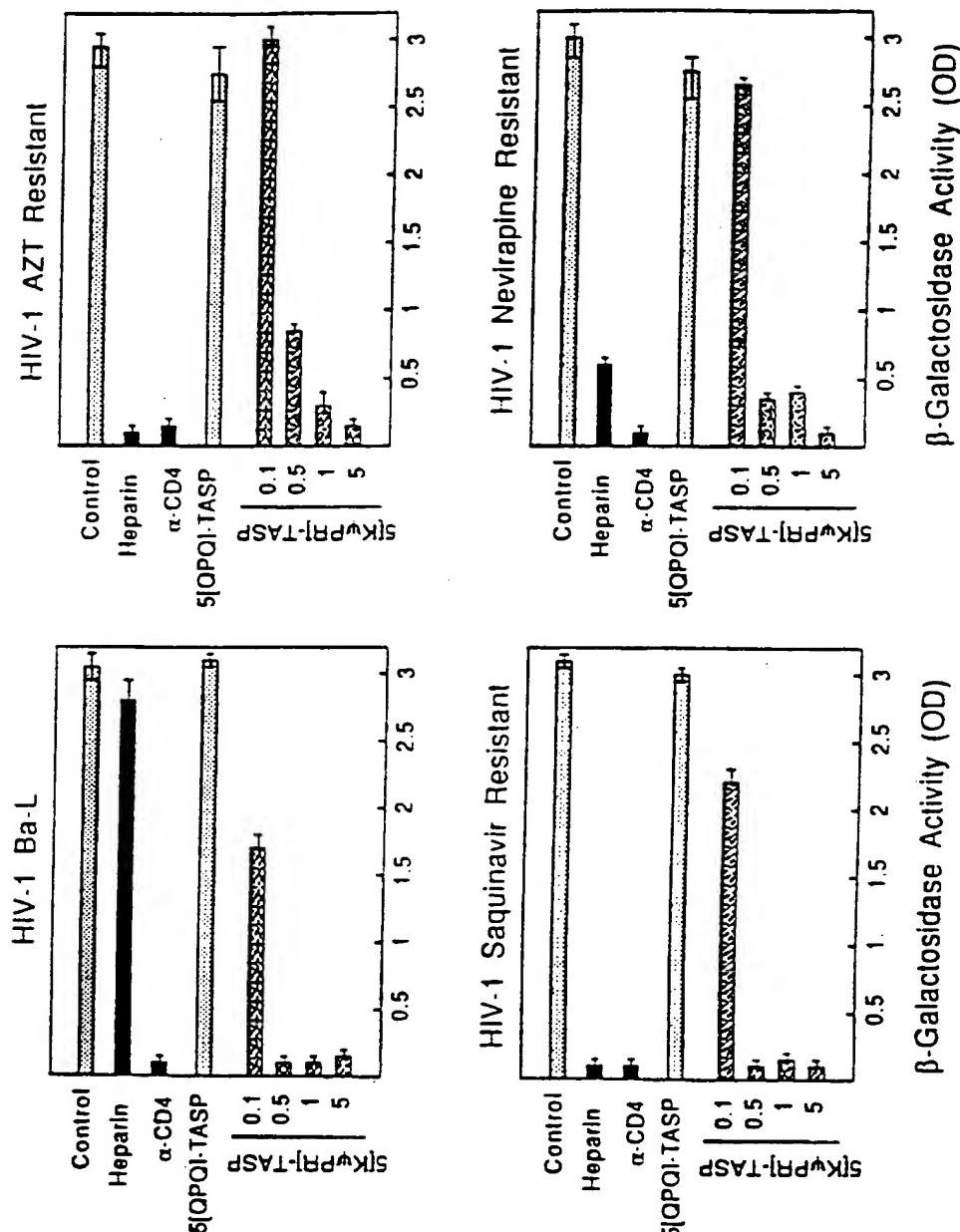


FIGURE 29

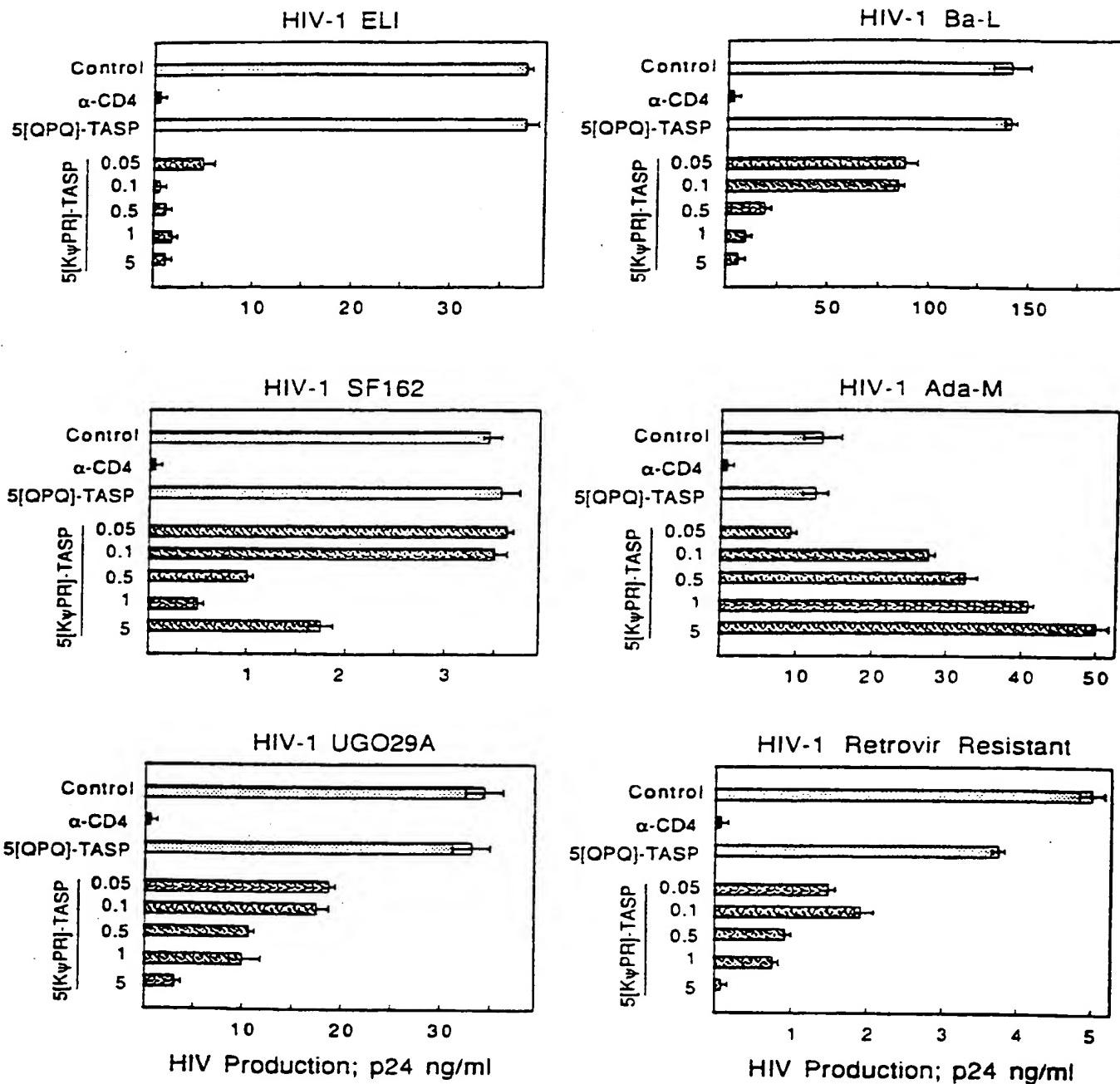


FIGURE 30

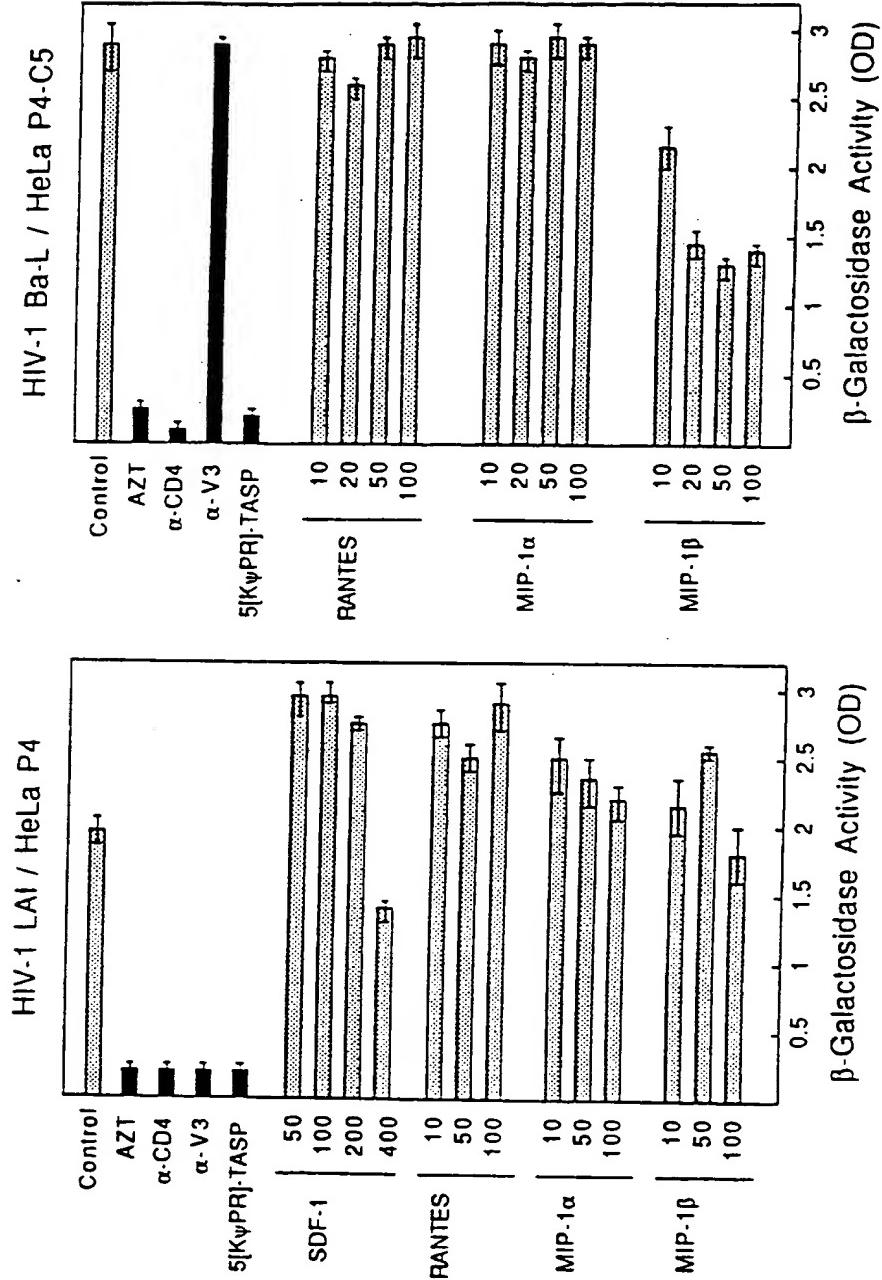


FIGURE 31

35 / 67

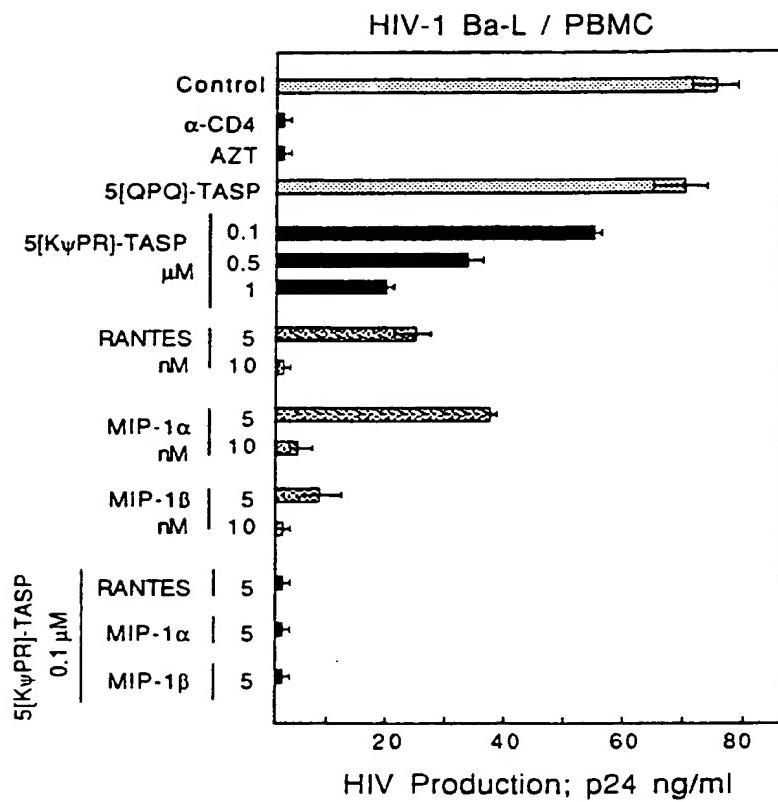


Figure 32

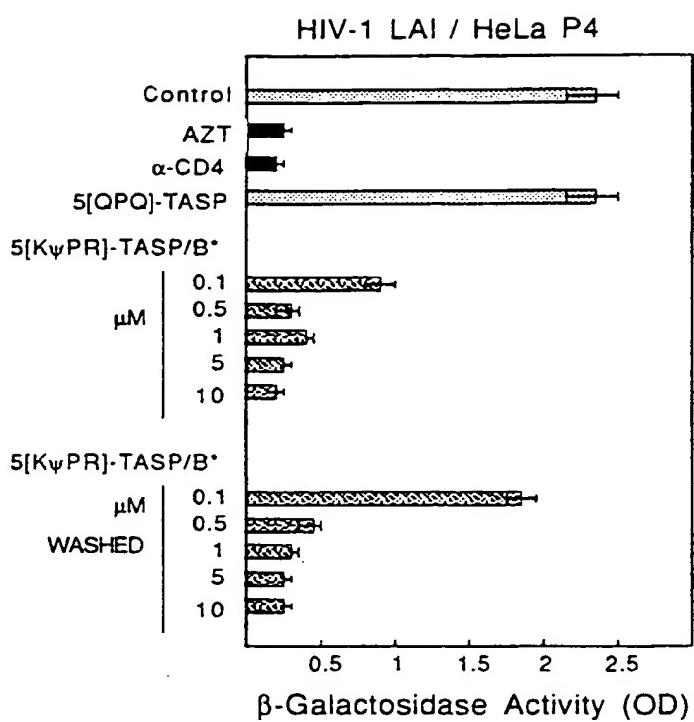


Figure 33

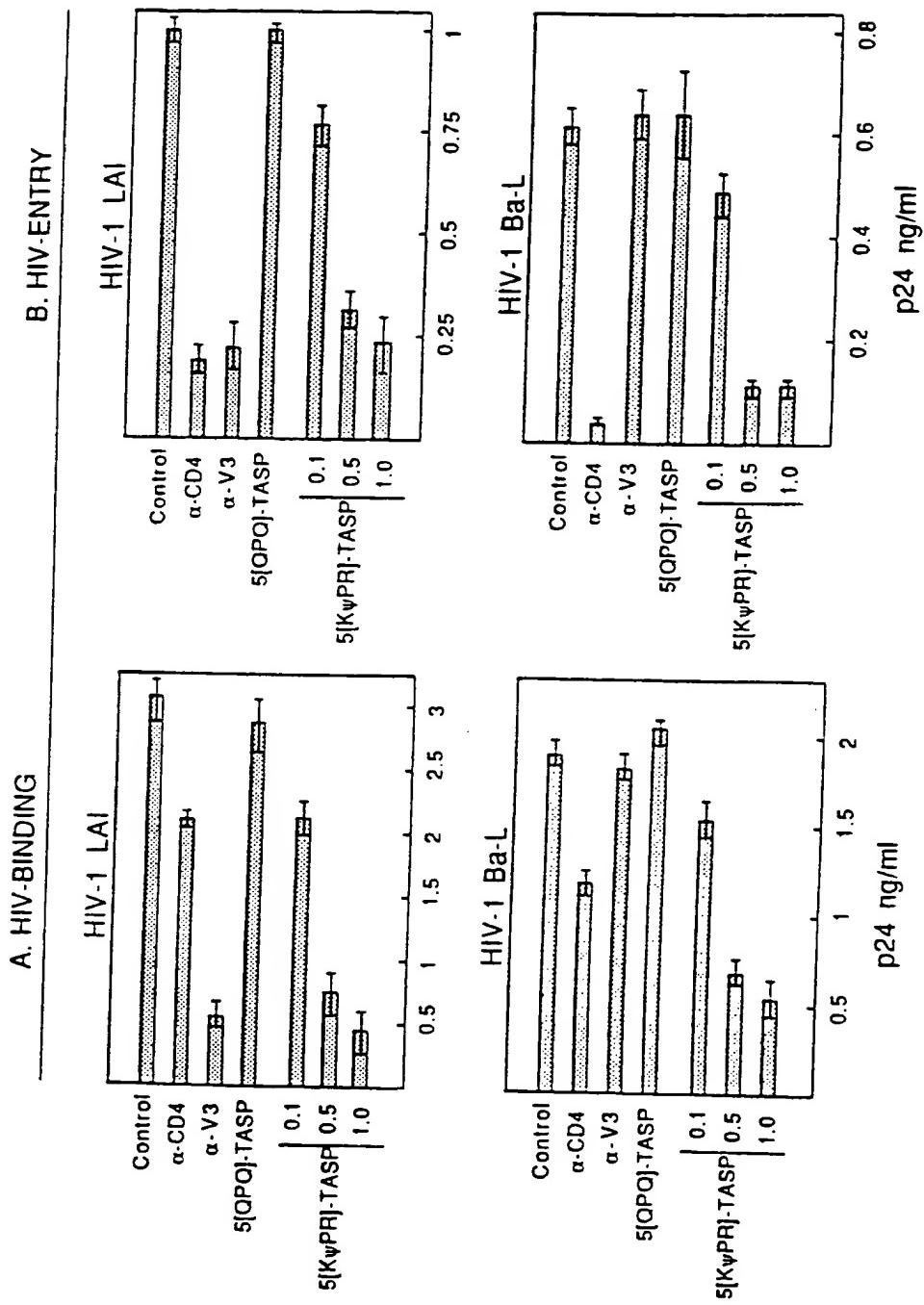


FIGURE 34

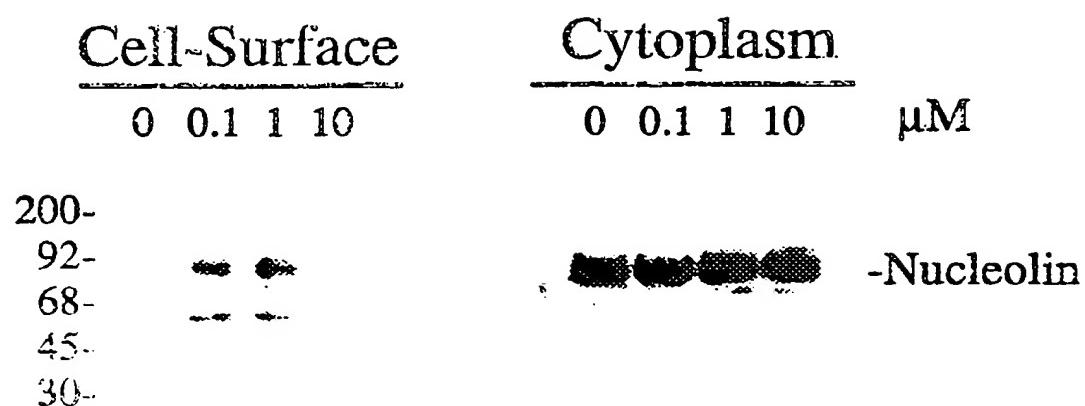


Figure 35

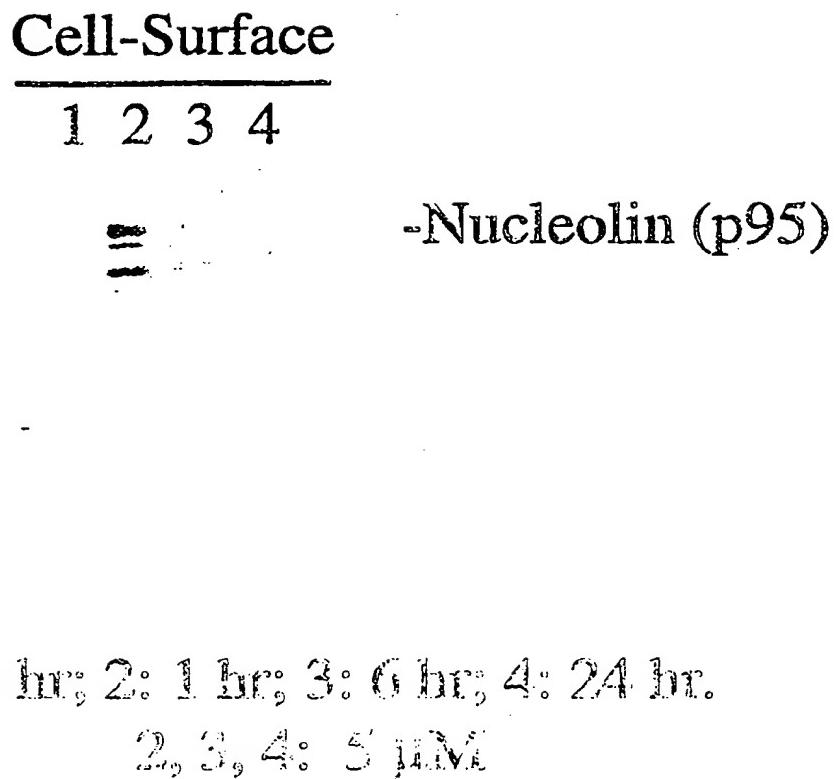


Figure 36

The effect of heparin at $\mu\text{g/ml}$ on HIV infection in HeLa P4-C5 cells.

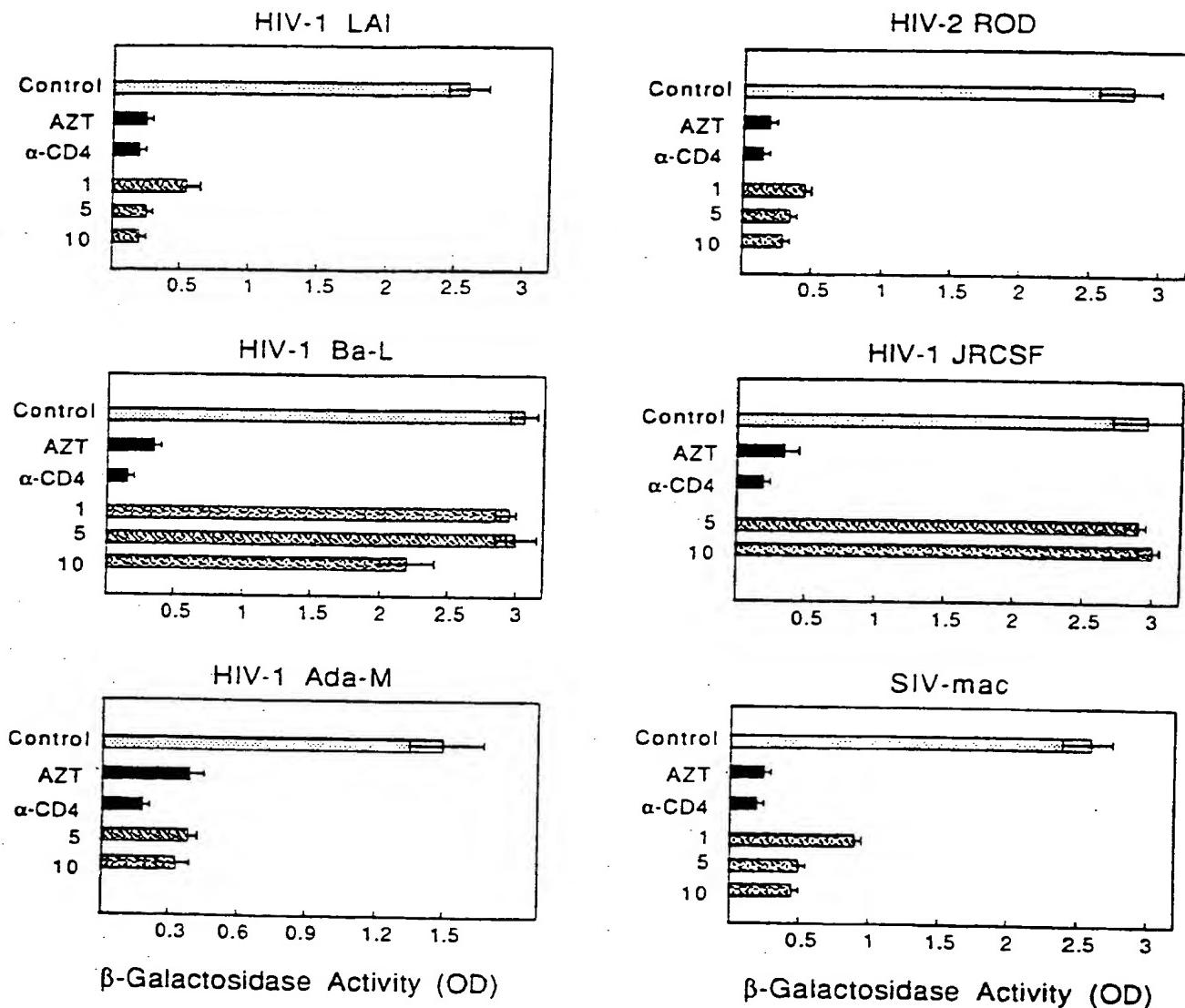


Figure 37

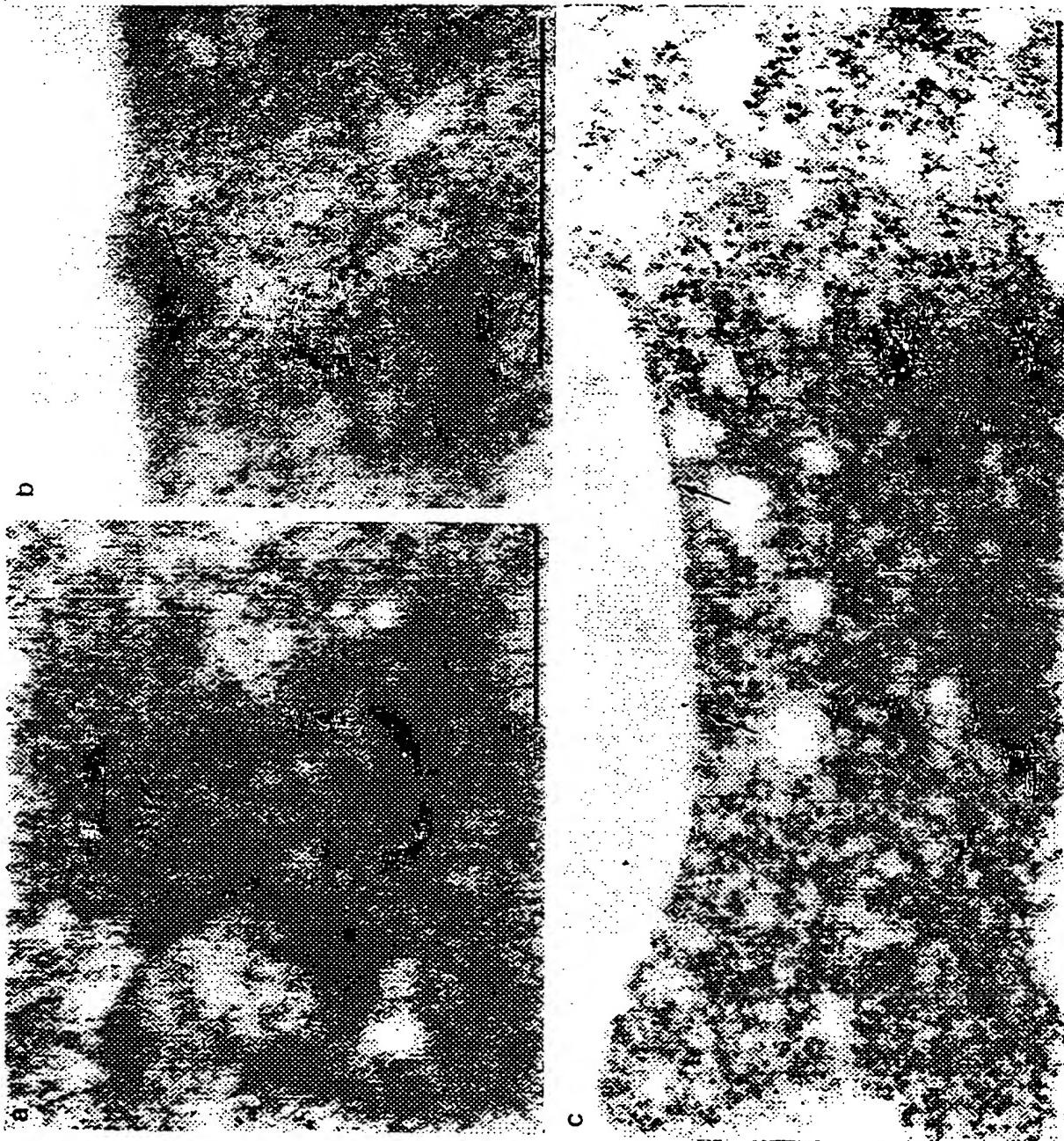


FIGURE 33

BEST AVAILABLE COPY



FIGURE 39

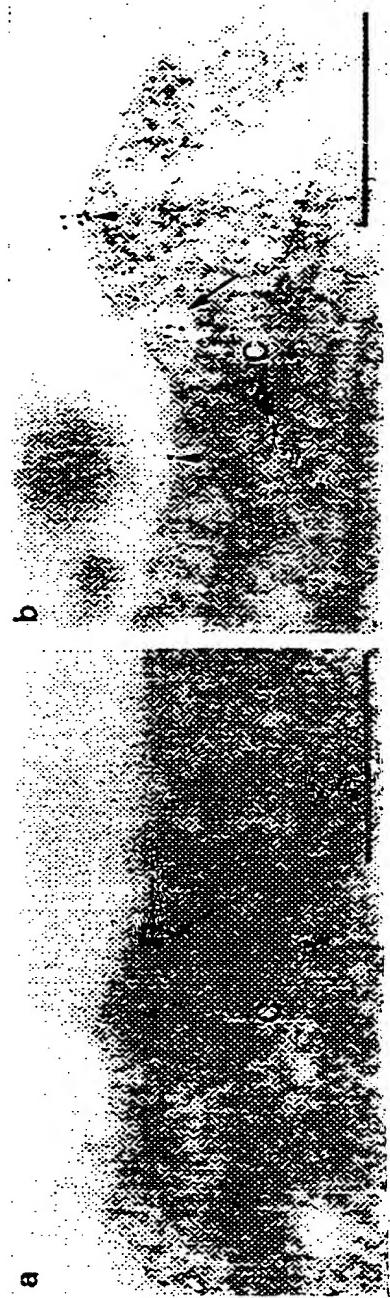


FIGURE 40A



FIGURE 40E

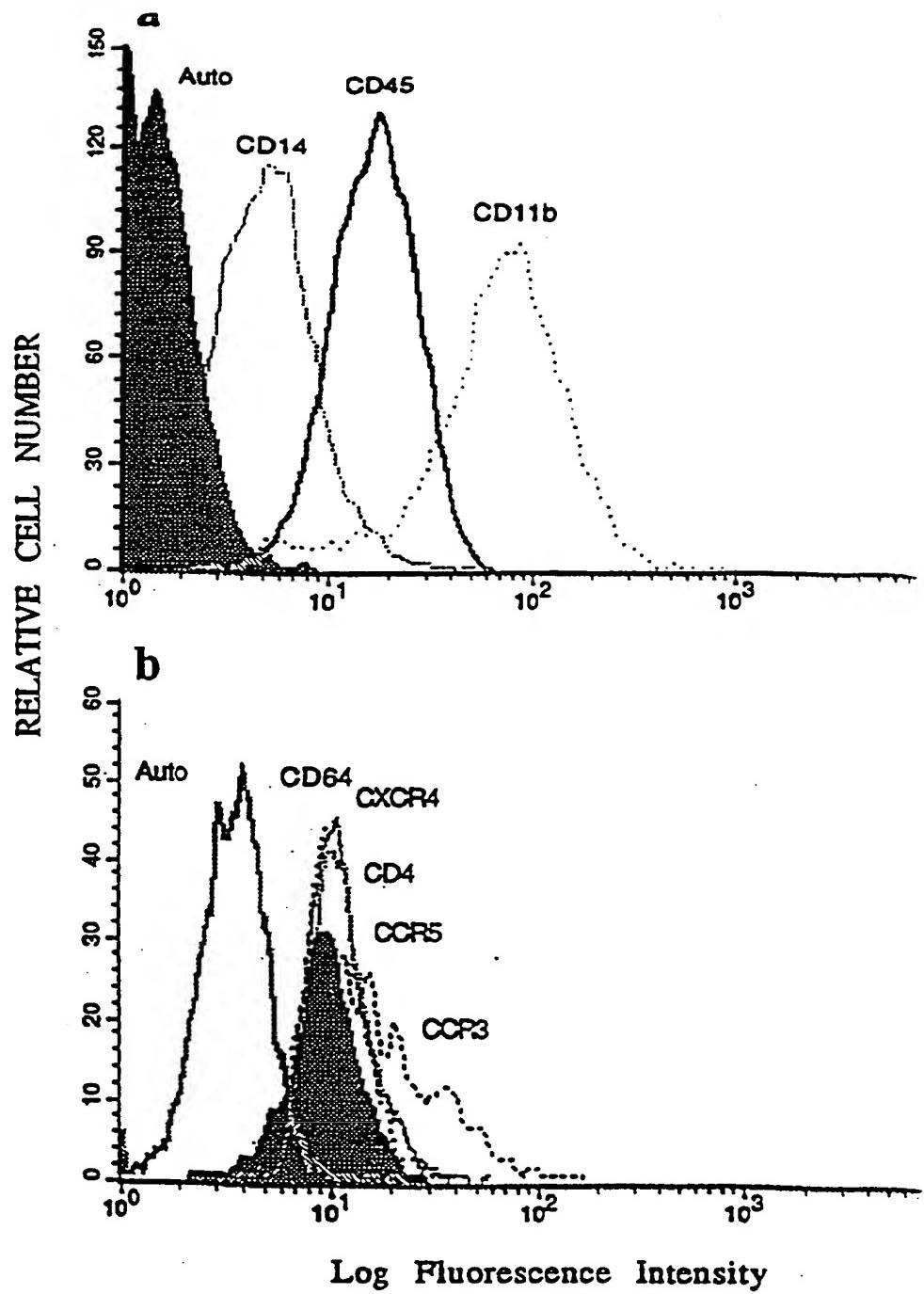


FIGURE 41

46 / 67

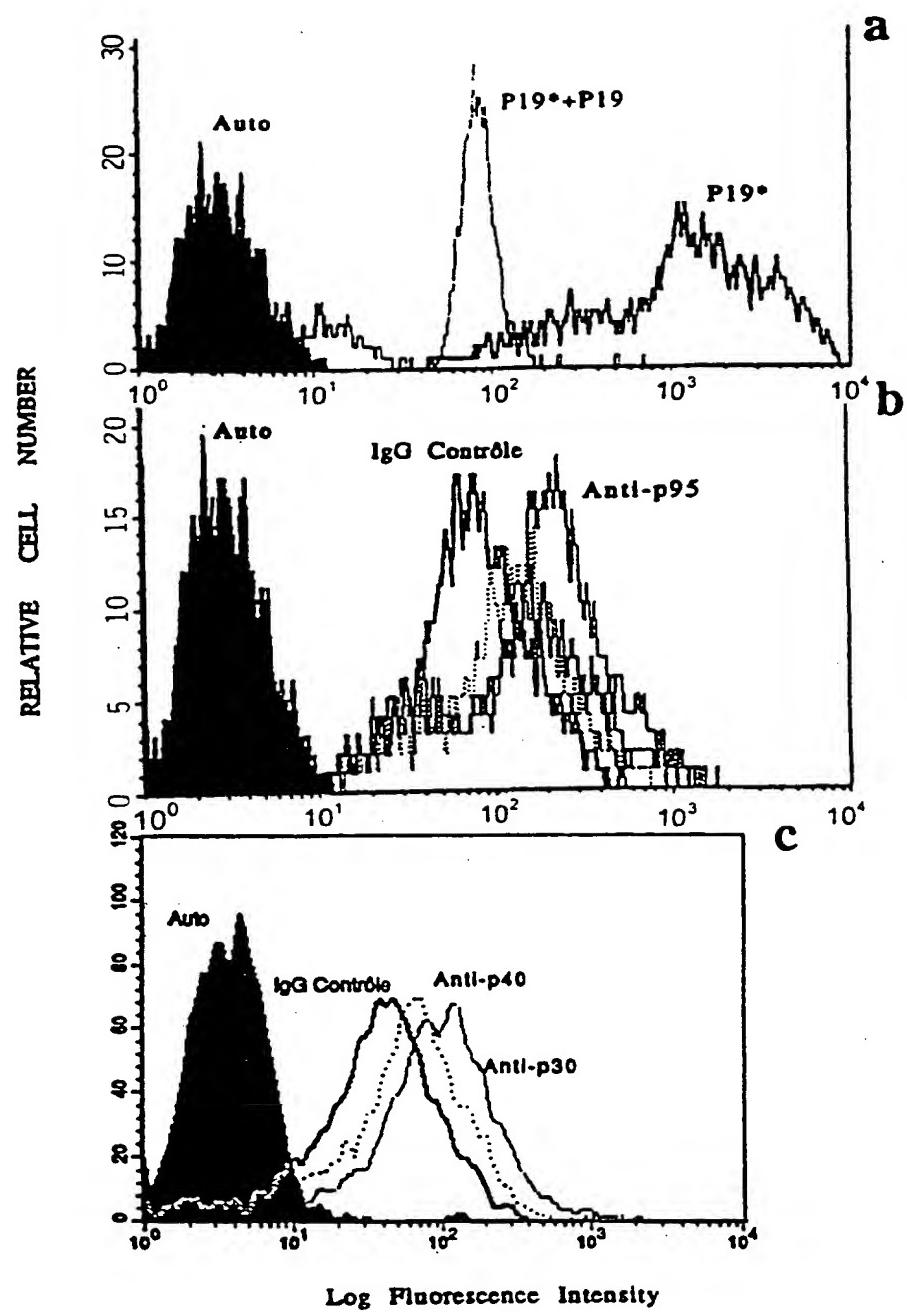


Figure 42

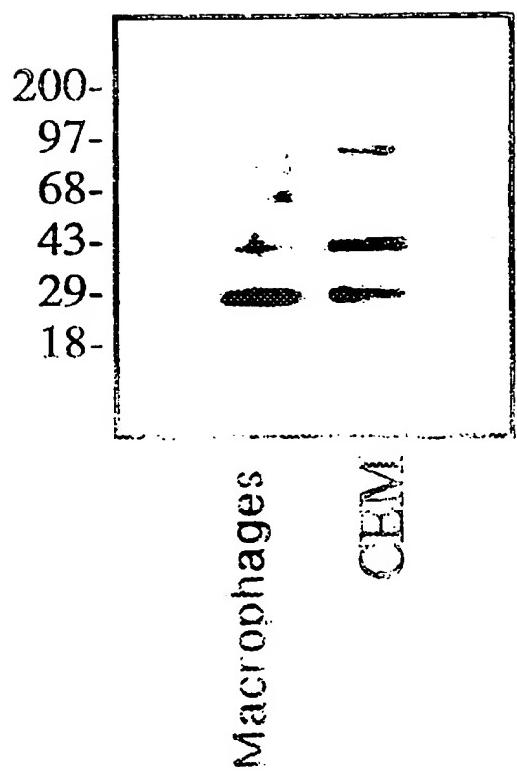


Figure 43

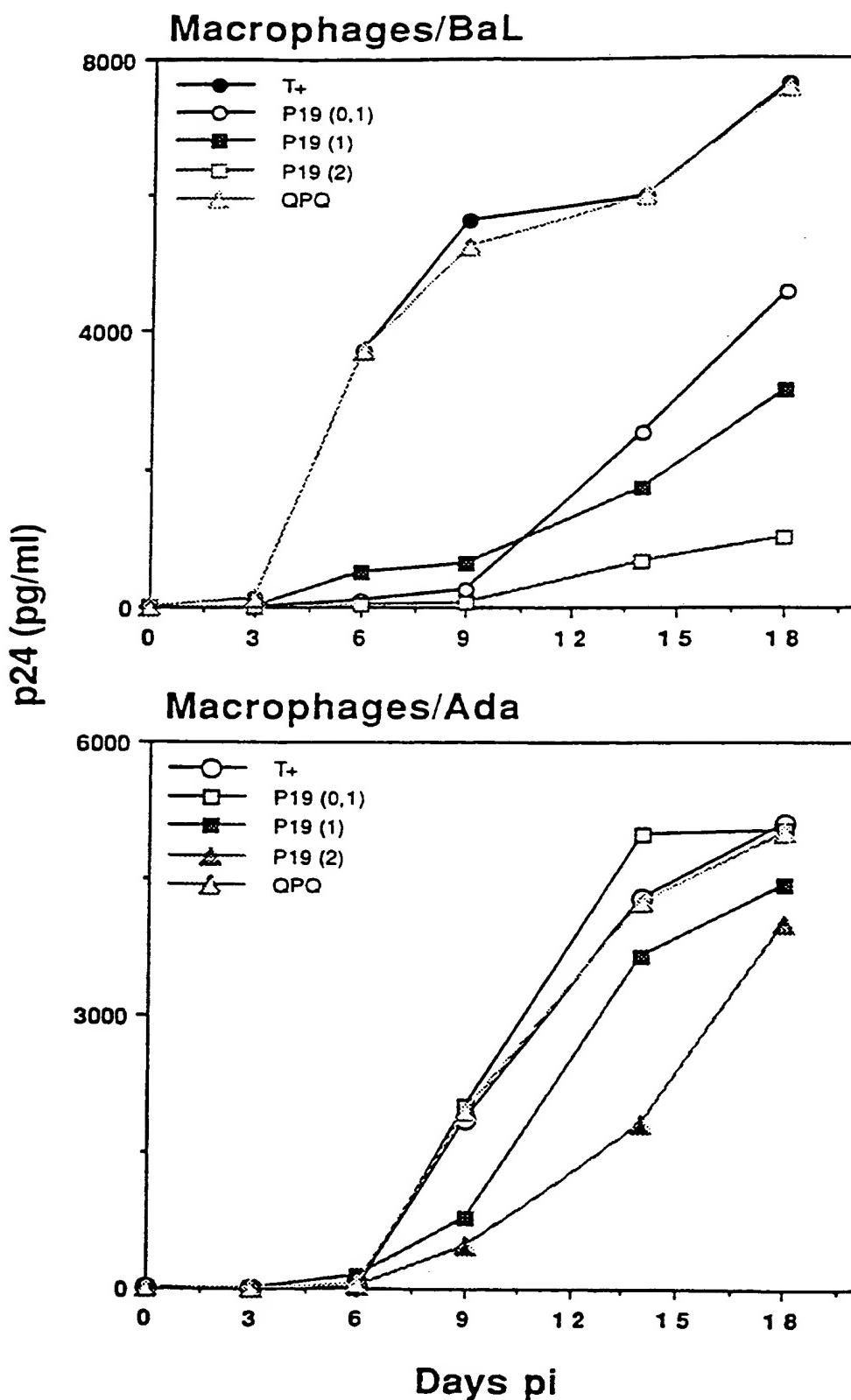


FIGURE 44
SUBSTITUTE SHEET (RULE 26)

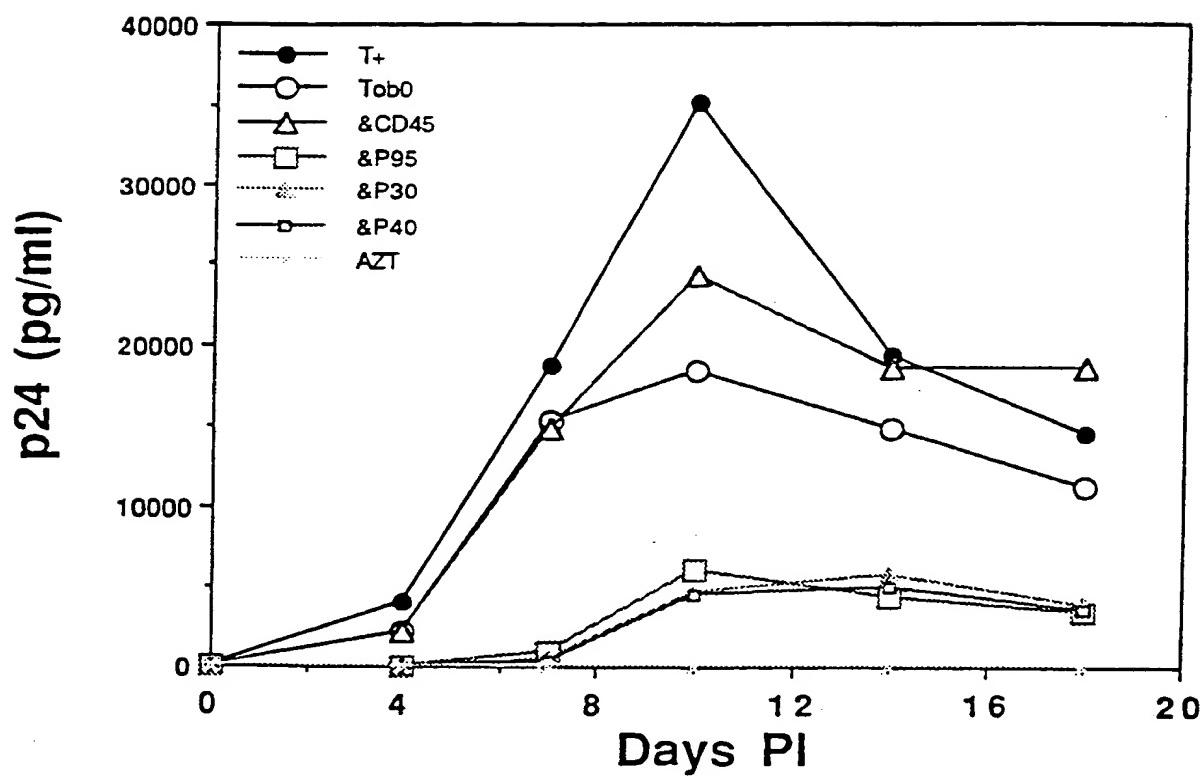
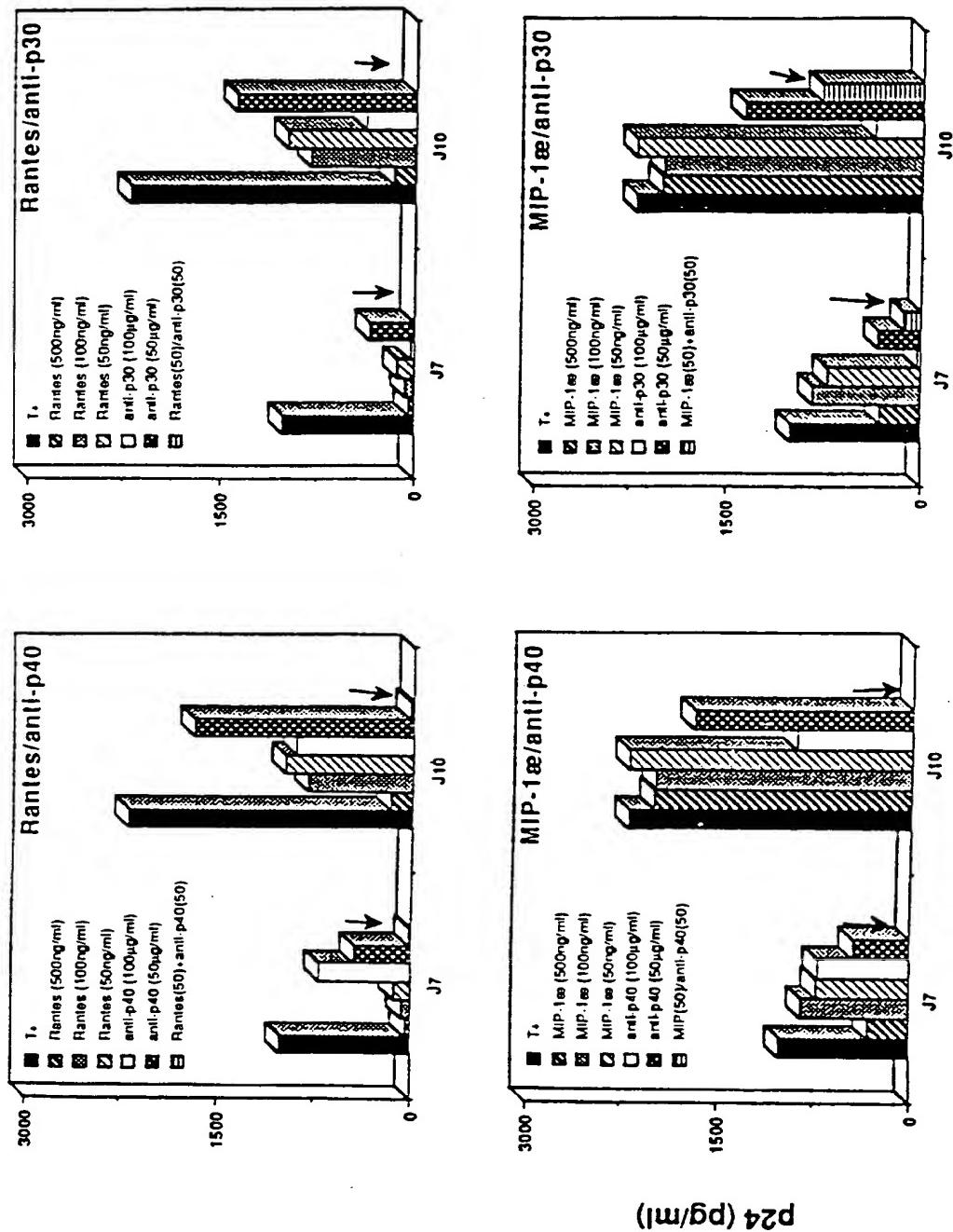


FIGURE 45



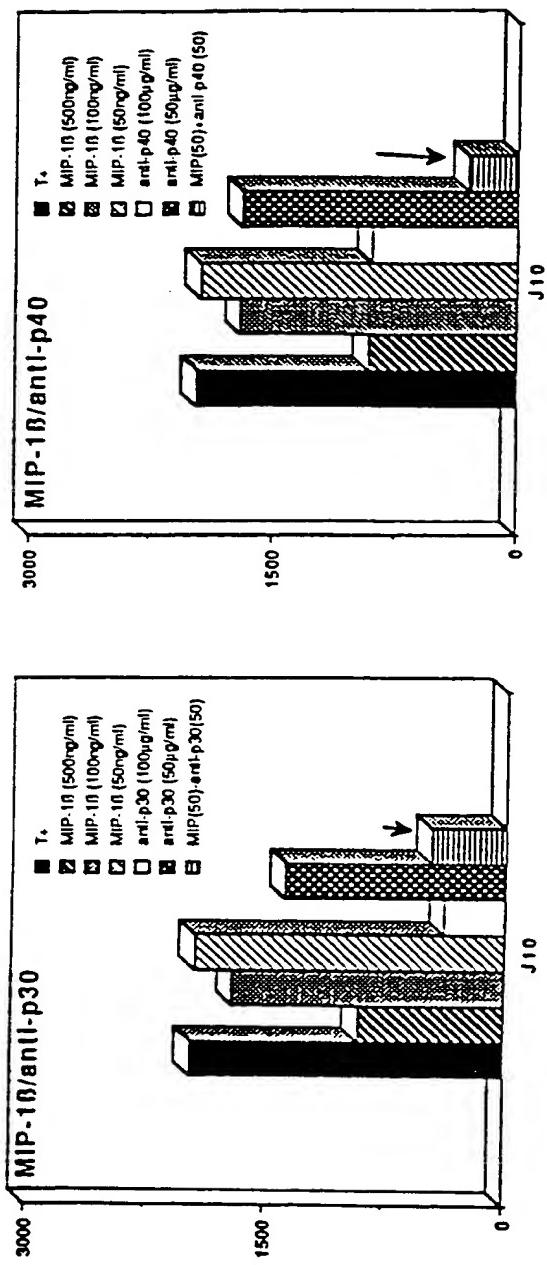


FIGURE 46B

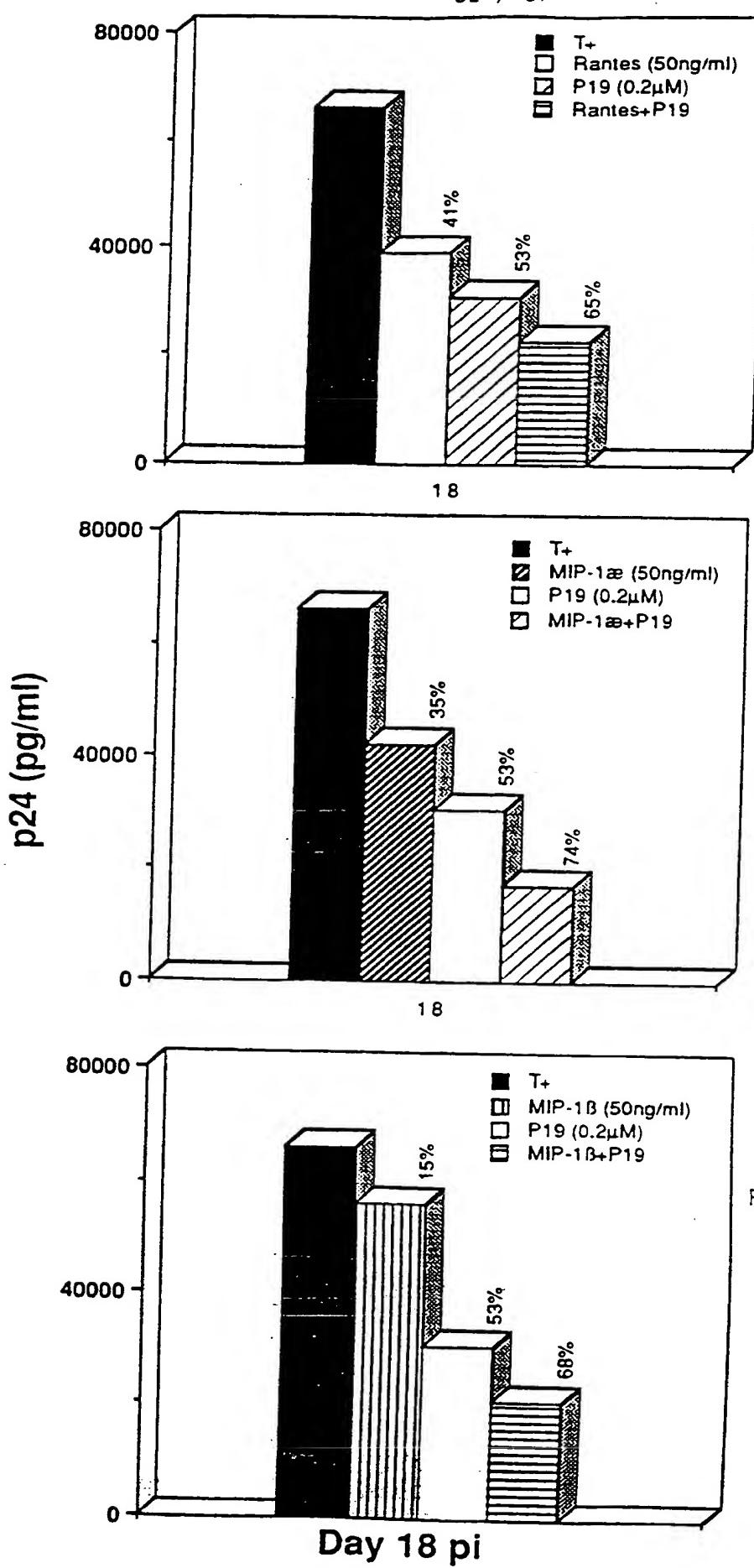


FIGURE 47

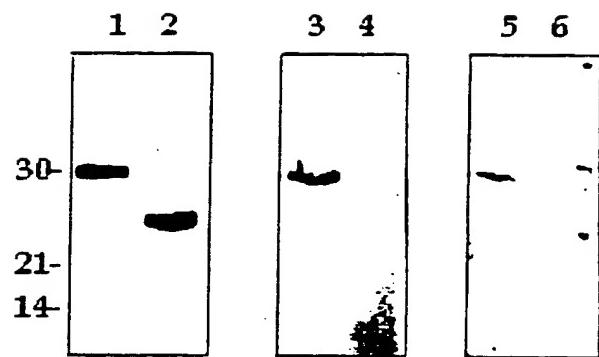


Figure 48

FIGURE 49(1)

I.

/translation="MVKLAAGKNQGDPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGE
EVVIPOKKGKAAATSAKVVSPTKKVAVATPAKKAATPGKKAATPAKKTVPACK
AVTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEEDDSEEDED
EDEDEDEDEIEPAAMKAAAAPASEDEDDEDDEDDEDDEDDEEEEEEPEVKEA
PGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKN
DLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVGNEIKLEPKGKDSSKERDA
RTLLAKNLPYKVTDDELKEVFEDAAEIRLVSKGSKGIAYIEFKTEADAETFEEKQ
GTEIDGRSISLYYTGEKGQNQDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEK
ATFIKVPQNQNGKSKGYAFIEFASFEADEALNSCNKREIEGRAIRLELQGPRGSPNA
RSQPSKTLFVKGLSEDTTEETLKESFDGSVRARIVTDRTGSSKGFGFVDFNSEEDAK
EAMEDGEIDGNKVTLDWAKPKGEGGFGGGRRGGFGGGRRGGFGGGRRGGFG
GRGGFRGGRRGGGDHKPQGKKTKEFQ"

II. 1 ATTCTGCTGT AGACATAGAG ATGATGATCA TAGCTGACTA TGATGATGAT

51 CCCCCGCGAG CCTGAAAGAG GAAATGCTCT GTTTGCTAA GCCCGCGAAT

101 CGAGTGAGAC CCACCCACAA AGCTAACCGT GGAAGTCACT GCGGGCCTCC

151 TTCGCCCTGC CAGCCGGGA ACCCATCCGG TGGCTCTCGA CCTGCTCCCG

201 GGCCATCTGG TGACACTGAC TTCGCAGCCA CCACCTTAAT TGGCGCATTG

251 GACCCAAATA ATAACCTGGG AACCTGTGGG CGGTCTAAGG CCCGGCTCTG

301 CGGTCGCCCT CCCAGGCCCC TCTCCCTGGC CCTGTGAGGC CAGAAAGTTA

351 CTTCTCCGAG GCCAGTTCCC CATGTCTGAG AAATATCTCC CAACTTGAGG

401 TTCTGTGGGG TAGGGGAGGG TTCGTGACTT TCTCACAGAA AACCTCGTAC

451 AGACCCCGCC ACTGCCTTTA TTAACAGCTC TCAGGAGACT GCCTGCAGGA

501 GGGGGTCGC TCCGGCCCCA TGCTCGCGGG CAAGCAGGGAA TAAGCTGTGC

551 CTCCAAAAGG GCCAACGGGA ACTCCCGGGT CCCTGAACCTT CCGGTGCTGG

601 AGGACTCCTC GCTCCAGGGC CACCAGGAGC CGCGGCGTGA GTGCGTGCCG

651 GAACCGAGGG CGGGGTCTCT GAGGAACCTCC AAGGCTGCC AAGCCTACGG

701 ACCCAGCCAC ATTGGCGAAC CGGAGACCGC CCGATTCCAC CACCCCCGCG

751 CTCCCTCAC AGCCGGCGCC AAAAACGCCA GTCCCACGAC GCAGGCCGGG

801 ACCCGCGCGC CCACGGCCCA ATCAGCGCGA CCTTGCACAA AGCGAGCCCC

FIGURE 49(2)

851 GCCCCCCACGG CGCCGTTGCC AGCCCCCTCCC CCTCCCGTGC CGCCTCGGCC
901 CGCCTACTCC CCGCCCCGCG CCGTTCACGG TTAGAGGCTC GCGATTGGCT
951 CATGGGGACG GCCGCGAGCT TTGGTTGGTC GGCGCGGAGT CACGAGGCAC
1001 CGTCGTGCC TTTCCACAGG CGTTACTGGG CAGGCTCAGT CTTTCGCCTC
1051 AGTCTCGAGC TCTCGCTGGC TTCGGGTGTA CGTGCTCCGG GATCTTCAGC
1101 ACCCGCGGCC GCCATCGCCG TCGCTTGGCT TCTTCTGGAC TCATCTGCGC
1151 CACTTGTCCG CTTCACACTC CGCCGCCATC ATGGTGAAGC TCGCGAAGGT
1201 AAACGGCCTT GAGCGCGACG CAGACGTGTA GGCTGCTTC CGAGGGCGA
1251 GCGCGGCGCC GCAGGGGAGGA GGGCCTGCGC GCAGTCCCGG GCGCGTTCTA
1301 GGGCGCCATG CTGCGGGAAG TCTCGCGCA TTAGTGGGA GGTCTCGCGC
1351 TTCTGGCTAC TTGGTGGCGA GGTGAAGAGC TTCTGCAGGT GCTGGGGAG
1401 GGGCGCTGG GCCTCGGGGT GGAGAGATGA GACCAAACCT TTGCGACGCG
1451 TACGAGCTGG GACTGACTCT GACGCACGTG CCCGGGAGCG TGCCCTGCCAC
1501 GTGGGCCGGC GTAGGTCTGG AATCTCCAGA GGGACCGGGT GCCTTGGGCC
1551 GGGAAATGGC GGTATCGGCC CTAGTCGGAG TCCCGGCTGC GCTCGGATGT
1601 CTCCGCCCG GCCTGGCAAG CCGATAACGTG GTGGGCCCG GAAGGTGGCT
1651 CTGCCCGTG CCTTTGCGC TGTGTTCGG GCAAGAGGTG GTCCCTGCCAG
1701 GTACCCCCAC GTGGCCGCAC CCGCCTCTT AAGGGCGGG GTAGTGCTGG
1751 GGAAAGGCAT AAGCTTCATG AGAAAATAAG GTAGTATTT TAAGTGCCTT
1801 AATGATCTTC ACCGTTAATT TGATTCAAAT AAGGGTGGTA GATAAAGTAC
1851 CGGGATTTGT AGTATAAAAA CACGGTTGTG CTTAACTAAG GTAACGGGAG
1901 GAGAAATCAT TTCCTCAGGT TGACTTTTA CCTTAGGGCA GGTTTCTGT
1951 TGGTAAAGCC TGGGAGGAAA AATGTGGCG GTTGAGAAGT AGTCCCTCTT
2001 GCATTGCCAT CAGGAGTAGT TTCTATGTTA GTTGTGGTGT TTGGCACTAT
2051 GAGAAATGAT CTGAGACGGA GATGATGGCG TATGAACACT AATGGCAAAA

FIGURE 49(3)

2101 TATGAATGGC CTGAAATGTC GAGGTGGAGG TGTAAATGATC TATTGTGTC
2151 CATTAGGC AGGTAAAAAT CAAGGTGACC CCAAGAAAAT GGCTCCTCCT
2201 CCAAAGGAGG TAGAAGAAGA TAGTGAAGAT GAGGAAATGT CAGAAGATGA
2251 AGAAGATGAT AGCAGTGGAG AAGAGGTAAT TTTATCCAAC TTAATGCAGA
2301 ATTATGTTAA AACTACAAAA TGAGAGTTA AGACATGAAA TTGGATATCT
2351 GTGGCAAAAA TAAGATTTA TCAGGTATGT CTTATTGTAG TGGTTGAGTG
2401 TTTCACAAAGC TCTTCATTGA CATGTCAAGA TGTCAATTGG CTAGTATTTG
2451 AATGTGAGTG CTAAGACGAG ACTGGGAATT TCTTTACAT GTTCCCTCTGC
2501 AGGGCTTGGG GTGTGATTTG TTGTGTTAAA TCATTACATT TTTCCAGTTT
2551 CAACATGTTA GCTCACCCCC ACATGTAGAG CTGGCATTG TATTCAAGAC
2601 TGAGAATAAC CTTACCAGAT TCCTTCCTA TCCTCCGAAT TAAAATTAAT
2651 TGGTCTCCAT TCCATATATA TATAACTGTA TCACTACTGG TTAAGTACTC
2701 GGGTAGAC TGAGGGCTGC CACCTCTCTT TGGTACCATT GACCCTCTTT
2751 AGCCACCTCC TGGCCTTTA TTTGCCTCCA CTATAAAGAC AGCTGAGCAC
2801 TGAATTGTC TCAGGTTTC GTTGAGAACC TGAATGAAAG TTTACTCTC
2851 CACACATTGC CTTGATAAAA CTACGGGATT TTAATGTAGC TAAATGATGA
2901 CTTTATCAA ACTACCATGC ACACCTTTG ATGTGTGATA GTTTGTAAG
2951 GAATATTTAT ATTTAGCCTA TTCATTTTT GTCTCAGGTC CTAAGAATTG
3001 AGCTTCACTG GGCTTGGTGG ACCGCAACCA CGAGGGCCCC AATGATTTAA
3051 TAAGTTAATG CTTGGAGCCT CCTATGTGTA ACGTTCTGAA TAATTTACAC
3101 ATAGCAATTG ATGACCTAA ACATGTAGG ATGATACTAT TACCAATTTC
3151 AGATGAGAAA GTGGGGCTT GGGAAAGTAT GAGGTGTAAG AATTCAAGAGG
3201 GTCTGGTCA GAGGTATTTT CAGTGTCAA AAGAGTTCT TATGTCTGGG
3251 TATTCACTT ATTATAGGGG CTCTGACTTA AGACAACATA ACAGAACGCT

FIGURE 49(4)

3301 GGAGTTTAA CATGTCATAT GTGTCAATGCG TATGTCTTGA ACCAGAGGCA
3351 TTGCCAGAGT CTAACAACTC ATTGGGACCA TGGTTATCTT TTTGGGTGTG
3401 GGGCTGGACT TACTGGTTG GTTTCAATT ATCTCAAGGT CGTCATAACCT
3451 CAGAAGAAAG GCAAGAAGGC TGCTGCAACC TCAGCAAAGA AGGTGGTCGT
3501 TTCCCCAACAA AAAAAGGTTG CAGTTGCCAC ACCAGCCAAG AAAGCAGCTG
3551 TCACTCCAGG CAAAAAGGCA GCAGCAACAC CTGCCAAGAA GACAGTTACA
3601 CCAGCCAAAG CAGTTACCAC ACCTGGCAAG AAGGGAGCCA CACCAGGCAA
3651 AGCATTGGTA GCAACTCCTG GTAAGAAGGG TGCTGCCATC CCAGCCAAGG
3701 GGGCAAAGAA TGGCAAGAAT GCCAAGAAGG AAGACAGTGA TGAAGAGGAG
3751 GATGATGACA GTGAGGAGGA TGAGGAGGAT GACGAGGACG AGGATGAGGA
3801 TGAAGATGAA ATTGAACCA CAGCGATGAA AGCAGCAGCT GCTGCCCTG
3851 CCTCAGAGGA TGAGGACGAT GAGGATGACG AAGATGATGA GGATGACGAT
3901 GACGATGAGG AAGATGGTAA GGAGTTGTCT TGGTAGTTAC TGGGCTTCTG
3951 ATTACAAGGT ATCTTGAGAT TCTGGGATCA CATATTCCCTT CATCGTACAA
4001 CCTGGAGATG AGATTAGAAT CTTGTGGAA TTCTCTTGGG TTGTTGTGGT
4051 GTGCTAGACT TAATTACCCA TGAATGATT TGTCTCTTG AGAAAATTTC
4101 AATAGCACAT CTATTAGTGT TTTTATAAT GTAGGATTT CGTTCTAAG
4151 TGATTTTTT TTTTTTTAA ATTTTTTGA GATGGAGCTT TTGCTGTTTC
4201 CCAGGCGGGA GTGCAATGGC GCGCTATCTC GGCCTACTGC AGCCTCCATC
4251 TCCTGGGTTTC AAGCAGTTCT GCCTCAGCCT CCCGAGTAGC GGGATTACAG
4301 GTGCCACCA CCACACCCCTA CTAATTTGT ATTTAGTAG AGACGACATT
4351 TCACCATGTT GGCCAGGCTG GCTCTGAAC TGTACCTCAG GTGATCCACC
4401 CACCTTAGGC TCTCCCAAAG TGCTAGGATT ACAGGTGAGA TATGCTGCGC
4451 CCGGCCCCAA GTGATCTATT CTTGCCATGA CTGTTAACTA AACATGGTGA
4501 CAGGATTGCA TTTCTTTAC ATTAGATTG AAAACCGATG TTGGTTTGG

FIGURE 49(5)

4551 GAGATTGCTG CAATTTTAG GTGACTTCTC TTTCAGACTC TGAAGAAGAA
4601 GCTATGGAGA CTACACCAGC CAAAGGAAAG AAAGCTGCAA AAGTTGTTCC
4651 TGTGAAAGCC AAGAACGTGG CTGAGGATGA AGATGAAGAA GAGGATGATG
4701 AGGACGAGGA TGACGACGAC GACGAAGATG ATGAAGATGA TGATGATGAA
4751 GATGATGAGG AGGAGGAAGA AGAGGAGGAG GAAGGTACTT AAATTAGATT
4801 CTGACATACG ACATGAGTTA TGTTAAAGG AGGCACTTAA GTGTTGTGG
4851 CTACTGATGT GTGATACATT GTTGACATC TTGTCCAGAG CCTGTCAAAG
4901 AAGCACCTGG AAAACGAAAG AAGGAAATGG CCAAACAGAA AGCAGCTCCT
4951 GAAGCCAAGA AACAGAAAGT GGAAGGTAAC TTGCAGAATT AGGGGATATG
5001 GGGGAGATAA ACAGCACAAA TGATGAATAA CAAAGGGACT TAATACTGAA
5051 ACCAGATGTT ACATTGTAGT GTGCTGATGT GCTGTGTATA GAAATTTGCG
5101 TTTGGAAACT AACTTTTAC CACACTACAA GTAGACTGAG TTGAGCTTTT
5151 TTTGTGCAGG CACAGAACCG ACTACGGCTT TCAATCTCTT TGTTGGAAAC
5201 CTAAACTTTA ACAAAATCTGC TCCTGAATTA AAAACTGGTA TCAGCGATGT
5251 TTTTGCTAAA AATGATCTTG CTGTTGTGGA TGTCAGAATT GGTATGACTA
5301 GGTAGCTGCT TCACTGCACG TTACATACCG TGGGTCTGTT AATTTTCCT
5351 TCCCCCTGTTA GCACAGTTAC TTTAGCCTGC CACTGTTAAA CATGAATACT
5401 GTAAACACTT CAAGGTTAGC ATTAGTGAAC TAAGTTAGAA TTAAACTGTA
5451 GATCCCCTAA GTTGCAATT CCATAATCAG TCGTAACCTG GTATAGCACA
5501 GAATAATTAA TAGTAATTAA TTTGTTGTT TTGTTATGTA TTGAGACGGA
5551 CGCTGGCTTT TGTTCAAGGCT GGAGTACAGT GGCGCAATCT TGGCTCACTG
5601 CAACCTCTGC CTCCCCGGTT CAAGCGATTC TCCTGCCTAA CCTCCCAAGT
5651 GACTGGGATA CGGGTGCCAC TCACCATGCA TGGCTAATT TTGTTTGTA
5701 TTTAGTATCG ATTCACCAT GTTGGTCGGC TGGTTTGAA CTCCTGACCT

FIGURE 49(6)

5751 CAAGTGATCC ACCCACCTCG GCCTCTCGAA GTGCTGGTAC AGCGTCACCA
5801 CCCTGCCAGT AAGTTTAAT AATTTGGTGT TAGGTGGGAG AATGCTTGAA
5851 CCTGGGAGGC AGAGGTTGCA GTGAGCCAAG TTCGCGCCAC TGTACTCCAG
5901 CCTGGGCAAC AGATTGAGAC ACCGTCTCAA TTTAAAATAA TGTTTATTTT
5951 CTTGGAAGTA CCTTGAAACT ATTAGACCTG TCTAGTCATC ATAGTGAATA
6001 CTTTATCCA GACAGGATT TCCTGTATTA GTGCTTATAG GTGTTCTTT
6051 GTCAGCTGCT ACTGTGAATT CTTATAAGCA ATTTAGCTCC ATGATGAAGA
6101 CCTCAAACGT GAATGTGCAT GTCATATCTT CATGCTGAGC CGTGTCTGT
6151 AGCTGCAGTT TGCAGAGCCT TGACTTTGTT TTGCTATACT AGGGGTGCTT
6201 TTTAAAATGT GATCTTTGTT TGCACCATCA CATTGTCTA GATACAGATT
6251 GTGATTTGA TTTGTGTTT CACCTGTTGT AATTTGCCC TCCTCTCCAC
6301 CTGAAGGAAA TTTGGTTATG TGGATTTGA ATCTGCTGAA GACCTGGAGA
6351 AAGCGTTGGA ACTCACTGGT TTGAAAGTCT TTGGCAATGA AATTAAACTA
6401 GAGAAACCAA AAGGAAAAGA CAGTAAGAAA GGTATGTAAG GCTTTATGAG
6451 TTATGCAATG AACTCAGGAG CTAGACTGCT AGGGAAAATG CTTTGTAAACC
6501 CATTCCCTT TGGTTCCCTC TTATTTTTT TAAATCATTT TTTCCCTTTG
6551 GTTCCTCTT AATGTGGAA TTAAATGAGC TACAGTGTGTT ACAAGGTACT
6601 TGGCACTGCT TGTCAGTGT AAGGTAAATT CCTGAGTTAG GCAAGCAAGA
6651 GCACTCTTAT ACAGAACAAAG AACCAATTACA TGCACCTAAA TTAAGCTAAG
6701 GATCTTCTT CACTGAAACT AGTTAGGTCC CTAATTACTC CCTATATACA
6751 GTGTAATGTT TTGAATTGGT ACATTCACTT TTTTGTTAT GCGCGTCTAC
6801 TCTAGGTTGA ACTCCAGTGT ACCTAACAGA GAGTTTGACA TCAAGGCTGT
6851 GACAACATGG AGGGACCACT TGTGTGTTGA CACTGCTATA TCTCCATATT
6901 TAGCACCGAG CCTTGTACAT ATAGGATCTC AAATTATTG TTGATAGAGC
6951 TATGTGTGTT TTTCCCTCT TTTGTTGTT GCCCCCCACC TTTGGTTTTT

FIGURE 49(7)

7001 CAGGCCACAG AGCTCATT TTATCTAGAGCG AGATGCGAGA
7051 ACACCTTTGG CTAAAAATCT CCCTTACAAA GTCACTCAGG ATGAATTGAA
7101 AGAAGTGT TTGAAGATGCTG CGGAGATCAG ATTAGTCAGC AAGGATGGGA
7151 AAAGTAAAGG GTATGTTCTT CTATTGAAAT GTAAGGGTTT TATTAACATT
7201 AATGCACTTC CTGCTTTATA AAAGAAATAT TGGTTTGATT TCCTTAGGCG
7251 TGTAACTTGG ACAGTTAAC CTGTAAGTTT GTGCCTCAGT AACCCATCTG
7301 TACCATGGGG ATAATGTACT CATAGGGTGA TTTTAAAAGA CAAAGCTAAT
7351 ACTTACAAAG AAGCAAGTTT AATGCCTATC TTACATAAAAT ACTTTGTAAG
7401 TAGTAGCAGT TCTTCAGTG AGGTGAGGTT ACATGAAAAA ATTCCAAGTA
7451 TTTGTAAAAC TAGTGGGAAG TAAGAGGGAA GCTCGAGTTT TGATTGAAAA
7501 GTGGACTAAA CAAGGGCATT TTATGTACTC AGATCTGAAG CAAGTTCTGT
7551 GTTGCTGAGG TAAAAGCATT TGTGTTAATA TGGTTTAAA AACCATGAGT
7601 TCTTCTCCCT CCATTGCAGG ATTGCTTATA TTGAATTAA GACAGAAGCT
7651 GATGCAGAGA AAACCTTGA AGAAAAGCAG GGAACAGAGA TCGATGGCG
7701 ATCTATTTCCT CTGTACTATA CTGGAGAGAA AGGTCAAAAT CAAGACTATA
7751 GAGGTGGAAA GAATAGCACT TGGAGTGGTA AGAAATTAGG CTTGTTCCAA
7801 GGTTTCAGA ATTGGTTGAG GGAACCTTC TAGTCTTGT ATTCATAAG
7851 TTTATAAATA CTTTTAATC AAAGTTACTC AAATGTAGGT GAAGATCAAG
7901 GACATGATAC CCCAAGTCAT ACTCTTATTT GGAATAGTAA TTTCCAATCT
7951 TGAAATGAGA GCTCTAAATC ATTTGCATT GGAATACAGT AGGCAAATCA
8001 AGCTTCCTT GTAGGCATGT TTTATACTTT AAATGACTTG ACCATGTGCC
8051 TTTTGAACTC AGATGATTCT AGGAAAACAG ACCAGTCATC AGCCTATGTA
8101 AGAACAAACCA GCAGGACATT GCAACACGTA CTAGGTACTT AATATGTTGA
8151 GTAACAGAAA TGGATTAGC TTACGTGATG AGTATTTGTA TATAACTCAA

FIGURE 49(8)

8201 GCACTGAAAT TCTTAGGGAA TAGATATTAC TGTTGTGACC GAAGCTGGGA
8251 CACTGTTCA GAGTCTTAGG AATGTGGCTC TCTATTCGA GGTGAATCAA
8301 AAACCTCTGGT TTTAAGCAAC CTCTCCTACA GTGCAACAGA AGAAACTCTT
8351 CAGGAAGTAT TTGAGAAAGC AACTTTATC AAAGTACCCC AGAACCAAAA
8401 TGGCAAATCT AAAGGGTAAG ATAATACCTT TGTATCATCA GTTATAGGCC
8451 TATATATGTC TTAGAGGTCT AAGGACGTAAG GGTATGTGT CCTGTAGAAA
8501 AAAGCTAAAT AATTTTAGCC TAGTAAATGA GTGTAAAATA AGTATATTTA
8551 GGTCCAACCT TGAGAGAAGG GCCTTGGCCA GATCATGTGA CCAGTGGTAT
8601 AGAGAGCATG TGCCTGGTAA ATTACTCTAA GCATTAACCG TTCATCCTCA
8651 GGTATGCATT TATAGAGTTT GCTTCATTG AAGACGCTAA AGAAGCTTTA
8701 AATTCCGTAA ATAAAAGGGA AATTGAGGGC AGAGCAATCA GGCTGGAGTT
8751 GCAAGGACCC AGGGGATCAC CTAATGCCAG AAGCCGTAAG TTCACCTGGT
8801 TAGGGTGCTG TGGTTGGGG TAGCACTCTC GGTGCTTTGT TTATTTTGC
8851 ACAAAATTCTG TGTTTCTGT TCGCTACTGA GTGAACAATA ACTGGATATC
8901 GATGACTGAT TACCTGAGAA ATAATTGATG AAATCTCAAG AAAATTCCCTC
8951 TAGATAGTCA AGTTCTGATC CAGCTGTCGT CAACTCAGAG TAGCAAGTTT
9001 GCCCATGATT TCCTGCCCA TCCACTGGGC CCCACCTGCT TGGGTTGCTT
9051 TCCCACCTTC CATAGAAGAC TGGGGCAGGA TATCAACTAT GCAATGGCAA
9101 TTAAAAAAATG TAAACCCAGA ATAGCCTTTA CTTTAATTAA GGACTAGTTG
9151 GCTTAGTTGC TTTTAACTGC TTTTCACTA TAACAAGTAT CTTGGCTAGT
9201 AGTCATACTA GGCATTGTGC AAATTCAGTG TACGAACTGT GAATTCACAT
9251 AAATCGAAA TTTTTTTTC CTTCCCAGAG CCATCCAAA CTCTGTTTGT
9301 CAAAGGCCTG TCTGAGGATA CCACTGAAGA GACATTAAG GAGTCATTTG
9351 ACGGCTCCGT TCGGGCAAGG ATAGTTACTG ACCGGGAAAC TGGGTCTCC
9401 AAAGGGTAAG GGAAGGAAGC GTGAGTGCTG CTTCCACTTG AAGGGTTTT

FIGURE 49(9)

9451 TGTTCTGTGC AGACCTTGAG TCTAATGTGT CTTCTCATTG AGCTCCTTCT
9501 GTCTATCAGT GGCAGTTTAT GGATTCGCAC GAGAAGAAGA GAGAATTCAC
9551 AGAACTAGCA TTATTTTACC TTCTGTCTTT ACAGAGGTAT ATTAGCTGT
9601 ATTGTGAGAC ATTCTGGGGT TCAAGCTGTC ACACCAGTTA GTTTCCATA
9651 GAGAGCTACT CTGCTGCACT GGTATCTTT TCCCAAATAA ACAAGGCTAC
9701 TTCTGTGGGA TGGCTCCCCA GCATGTACAG TTAACTTGGG ACATGTGTAG
9751 TAGGTGCTTT TTATAATGGG CAATTCATT TGGTGTCTA GGTTTGGTTT
9801 TGTAGACTTC AACAGTGAGG AGGATGCCAA GGAGGCCATG GAAGACGGTG
9851 AAATTGATGG AAATAAAGTT ACCTTGGACT GGGCCAAACC TAAGGGTGAA
9901 GGTGGCTTCG GGGGTCGTGG TGGAGGCAGA GGCGGCTTTG GAGGACGAGG
9951 TGGTGGTAGA GGAGGCCGAG GAGGATTGG TGGCAGAGGC CGGGGAGGCT
10001 TTGGAGGTAA GGCACGCAGA GATAATGACA CCACATAGCA TGTGCTCTTC
10051 AGACCCTGTG CCCTGTCACG GTTCCTAATC ACTGGGGAGG AGGAGCTTTG
10101 TACCCATTCT TTTAACAGTG TCTTGCCTTC CTCCTGTAGG GCGAGGAGGC
10151 TTCCGAGGAG GCAGAGGAGG AGGAGGTGAC CACAAGCCAC AAGGAAAGAA
10201 GACGAAGTTT GAATAGCTTC TGTCCCTCTG CTTTCCCTTT TCCATTTGAA
10251 AGAAAGGACT CTGGGGTTTT TACTGTTACC TGATCAATGA CAGAGCCTTC
10301 TGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT TGGAAATCCG
10351 TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTTGA CTGGATATTG
10401 ATATAAAACTT TTTAAAGAGT TGAGTGATAG AGCTAACCT TATCTGTAG
10451 TTTTGAATT ATATTGTTTC ATCCCATGTA CAAAACCATT TTTCCTACA
10501 AATAGTTGG GTTTGTTGT TGTTACTTTT TTTTTGTTT TTGTTTTTT
10551 TTTTTTGCG TTCGTGGGGT TGTAAAAGAA AAGAAAGCAG AATGTTTTAT
10601 CATGGTTTTT GCTTCACCGC TTTAGGACAA ATTAAAAGTC AACTCTGGTG

63 / 67

FIGURE 49(10)

10651 CCAGACGTGT TACTTCCTAA AGAGTGTTC CCCTGGAATC TCACTGGAGA
10701 GCATGGCAA A GCCAGCTCTG CCACTTGCTT CACCCATCCC AATGGAAATG
10751 GCTTAGTGCG TGTTTCCAGT ATCCCAGCCC TAACTAACCTT GGTTGAAATG
10801 CTGGTGAGGG GACCTGCTCC TGCAGCCCTG GTGCTGACTT GAAGGCTGCT
10851 GCAGCTTCTC CTACTTTAG CAGGTCTCGA GGATTATGTC TGAAGACCAC
10901 TCTGGAAAGA GGTGAGGAA CAGATTAGTC AGGTTTCCTA GG

FIGURE 49(11)

III.

"MEMGRRIHLELRNRTPSDVKELVLDNSRSNEGKLEGLTDEFEL
EFLSTINVGLTSIANLPKLNKKLELSDNRVSGGLEVLAEKCPNLTHLNLSGNKIKD
LSTIEPLKKLENLKSLDLFNCEVTNLNDYRENVFKLLPQLTYLDGYDRDDKEAPDSDA
EGYVEGLDDEEEDEEEYDEDDAQVVEDEEDEDEEEGEEEDVSGEEEEDEEGYNDGE
VDDEEDEEEELGEEERGQKRKREPEDEGEDDD"

FIGURE 49(12)

III.

1 GCTGGTTGAG CCTTCAAAGT CCTAAAACGC GCGGCCGTGG GTTCGGGGTT
51 TATTGATTGA ATTCCGCCGG CGCAGGAGCC TCTGCAGAGA GAGAGCGCGA
101 GAGATGGAGA TGGGCAGACG GATTCAATTAA GAGCTGCGGA ACAGGACGCC
151 CTCTGATGTG AAAGAACCTTG TCCTGGACAA CAGTCGGTCG AATGAAGGCA
201 AACTCGAAGG CCTCACAGAT GAATTGAAAG AACTGGAATT CTTAAGTACA
251 ATCAACGTAG GCCTCACCTC AATCGCAAAC TTACCAAAGT TAAACAAACT
301 TAAGAACGCTT GAACTAACGCG ATAACAGAGT CTCAGGGGGC CTGGAAGTAT
351 TGGCAGAAAAA GTGTCCGAAC CTCACGCATC TAAATTAAAG TGGCAACAAA
401 ATTAAAGACC TCAGCACAAT AGAGCCACTG AAAAAGTTAG AAAACCTCAA
451 GAGCTTAGAC CTTTCAATT GCGAGGTAAC CAACCTGAAC GACTACCGAG
501 AAAATGTGTT CAAGCTCCTC CCGCAACTCA CATATCTCGA CGGCTATGAC
551 CGGGACGACA AGGAGGCCCG TGACTCGGAT GCTGAGGGCT ACGTGGAGGG
601 CCTGGATGAT GAGGAGGAGG ATGAGGATGA GGAGGAGTAT GATGAAGATG
651 CTCAGGTAGT GGAAGACGAG GAGGACGAGG ATGAGGAGGA GGAAGGTGAA
701 GAGGAGGACG TGAGTGGAGA GGAGGAGGAG GATGAAGAAG GTTATAACGA
751 TGGAGAGGTA GATGACGAGG AAGATGAAGA AGAGCTTGGT GAAGAAGAAA
801 GGGGTCAGAA GCGAAAACGA GAACCTGAAG ATGAGGGAGA AGATGATGAC
851 TAAGTGGAAT AACCTATTTT GAAAAATTCC TATTGTGATT TGACTGTTT
901 TACCCATATC CCCTCT

FIGURE 49(13)

IV.

"MSAPAAKVSKKELNSNHDGADETSEKEQQEAIEXHIDEVQNEIDR
LNEQASEEILKVEQKYNKLQPFFOKRSIELIAKIPNFVWTFVNHPQVSALLGEEDEE
ALHYLTRVEVTEFEDIKSGYRIDFYFDENPYFENKVLSEFHNLNESGDPSSKSTEIKW
KSGKDLTKRSSQTQNKAASKRQHEEPESFFTWFDTDHSAGADELGEVIKKDDIWPNPLQ
YVLVPDMDEEGEDEGGEDDDDEEEEGLEDIDEEGDEGEDEGGEDDDDEGEDEGGED
D"

IV.

1 CGACCGCGGA GCAGCACCAT GTCGGCGCCG GCGGCCAAAG TCAGTAAAAA
51 GGAGCTCAAC TCCAACCACG ACGGGGCCGA CGAGACCTCA GAAAAAGAAC
101 AGCAAGAAC GATTGAACAC ATTGATGAAG TACAAAATGA AATAGACAGA
151 CTTAATGAAC AAGCCAGTGA GGAGATTTG AAAGTAGAAC AGAAATATAA
201 CAAACTCCGC CAACCATTTC TTCAAGAAGAG GTCAGAATTG ATCGCCAAA
251 TCCCCAAATT TTGGGTAACA ACATTTGTCA ACCATCCACA AGTGTCTGCA
301 CTGCTTGGGG AGGAAGATGA AGAGGCCTG CATTATTTGA CCAGAGTTGA
351 AGTGACAGAA TTTGAAGATA TTAAATCAGG TTACAGAATA GATTTTTATT
401 TTGATGAAAA TCCTTACTTT GAAAATAAAG TTCTCTCCAA AGAATTTCAT
451 CTGAATGAGA GTGGTGATCC ATCTTCGAAG TCCACCGAAA TCAAATGGAA
501 ATCTGGAAAG GATTGACGA AACGTTCGAG TCAAACGCAG AATAAAGCCA
551 GCAGGAAGAG GCAGCATGAG GAACCAGAGA GCTTCTTTAC CTGGTTTACT
601 GACCATTCTG ATGCAGGTGC TGATGAGTTA GGAGAGGTCA TCAAAGATGA
651 TATTTGGCCA AACCCATTAC AGTACTACTT GGTTCCCGAT ATGGATGATG
701 AAGAAGGAGA AGGAGAAGAA GATGATGATG ATGATGAAGA GGAGGAAGGA
751 TTAGAAGATA TTGACGAAGA AGGGGATGAG GATGAAGGTG AAGAAGATGA
801 AGATGATGAT GAAGGGGAGG AAGGAGAGGA GGATGAAGGA GAAGATGACT
851 AAATAGAACCA CTGATGGATT CCAACCTTCC TTTTTTAAA TTTCTCCAG
901 TCCCTGGGAG CAAGTTGCAG TCTT

V.

C'TCGGGTTACGTGCTCCGGATCTTCAGCACCCGGCATCGCCGAGGCTCGCTGGCTTCTGGACTCATCTGCG
 CCACCTGGCCATTCAACTCCGGCCTTGCTGAAGATACTGAGAATGAGAATGAGGCTGCTGCACCTCAGCAGAAAGGTA
 TGGCTCCTCCAAAGGGAGGTAGMGAAGATACTGAGAATGAGAATGAGGCTGCTGCACCTCAGCAGAAAGGTA
 GAAGGGTGCAGTTGCCAACCCAGCCAGGAGGCTGCTGCACCTCCAGGAGGAGGCTGCTGCACCTCAGCAGAAAGGTA
 CAGTTACACCCAGCCAAAGGGCAAGGAGGTACCCACACCTGGCAGGAAGGGAGGAGGCTGAGGAGGAAAGGAGGAGG
 AAGAAGGGTGCATCCAGCCAGGAGGAGGCTGCTGCAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 TGATGACAGTGAGGGATGAGGGATGAGGGAGGAGGATGAGGGATGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 CAGCAGCTGGCTGCCCTGCCTCAGGGATGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 GATGACTCTGAAGAAGAGCTATGGACTACACCAAGCCAAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 ATGATGAAGATGATGAGGGAGGATGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 ATGGCCAAACAGAAAGGAGCTCCCTGAAGCCAAAGAAACAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 TGTTGGAAAACCTAAACAAATCTGCTCTGAAATTAAACTGGTATGACTAGGAATTGGTATTGGAATTAAAGCAGAAAGGAGG
 CTGTTGGATGTCAGAATTGGTATGACTAGGAATTGGTATTGGAATTAAAGCAGAAAGGAGGAGGAGGAGGAGGAGG
 TTGGAAACTCAGCTGGTTGAAGACTTGGCTAAACAAATCTCCCTAACAGTCACTCAGGATGGTATTGGAATTAAAGCAGAAAGG
 AGATGGGAGAACACTTTGGCTAAACAAATCTCCCTAACAGTCACTCAGGATGGGAAAGTAAGGGATGCTTATATTGAATTAAAGCAGAAAGG
 CGGAGATCAGATTAGTCAGCAAGGATGGGAAAGTAAGGGATGCTTATATTGAATTAAAGCAGAAAGGAGGAGGAGGAGGAGG
 AAAACCTTTGAAGAAAAGCAGGAAACAGAGATCGATGGGGGATCTTCCCTGACTTACCTGGTTTAAGCAGAAAGGAGGAGGAGG
 TCAGACTATAGGGTGAAGAATAGCATTGGAGTGGGTGAATTCAAAGTCAACTTTATCAAAGTACCTTAAAGCAGAAAGGAGGAGGAGG
 GGGTATGCATTATAGAGTTGGCTTCATTGAGAGCCTAAAGGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAGG
 CAGAGCAATCAGGTGGAGTTGCAAGGACCAGGGGATCACCTTATGCCAGAAGCCAGGCTCCCTGGGCAAGGAGGAGGAGGAGGAGG
 AAGGGCTGCTGAGGATACCCTGAAGAGACATTAAAGGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAGCTTAAAGGAGG
 CGGGAAACTGGGTCTCCAGG
 TGAAATTGATGAAATAAGTTACCTGGACTGGGCAACCTTAAGGGTGAAGGTGCTGGGTTTACTGTTACCTGATCAGTGA
 GAGGGGGCTTGGAGG
 CGAGGAGGCTTCCAGG
 GTCCTCTGCTTCCCTTCCATTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 GAGGAGCATTCAAGACAGTACAGTCCTGGTGGCTCCCTGGAAATTCCGCTCTAGTTAACATTCAAGGAGGAGGAGGAGGAGG
 TCGTTTGACTGGATATCATATAAACTTAAAGAGGTTGAGTATAGAGCTMCCCTTATCTGTMAGTTT;AATTTA
 TAT1GTTGACTCCCATGTCACAAA:CCATTTCCTAC